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GenCore version 5.1.6
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; Search time 3 Seconds (without alignments)
1.084 Million cell updates/sec - nucleic search, using sw model 2, 2003, 15:45:58 October OM nucleic Run on:

1 agggattcaggggttccagc us-09-676-436-3 20 Title: Perfect score: Sednence:

7024 seqs, 81329 residues Searched:

IDENTITY_NUC Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8 Maximum DB seq length: 50

Maximum Match 100% Listing first 32 summaries Post-processing: Minimum Match 0%

rnpb.seg:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1270, Ap 1275, Ap 1275, Ap 1270, Ap 1275, Ap 1337, Ap 1337, Ap 1496, Ap 1270, Ap 1270, Ap 68, Appl 67, Appl 11, Appl 26, Appl 18, Appl Sequence 12, Description Sequence Seguence Sequence Sednence Sequence Sequence Sequence US-10-371-474-64
US-10-371-474-64
US-09-953-562-23
US-09-953-562-24
US-09-953-562-24
US-10-371-474-61
US-09-953-562-24
US-09-953-562-1
US-09-953-562-1
US-09-953-562-1
US-09-953-562-1
US-09-953-562-1
US-09-991-486B-67
US-09-991-486B-67
US-09-991-486B-67
US-09-991-486B-67
US-09-991-186-127
US-10-330-627-435
US-10-330-627-435
US-10-330-627-588
US-10-331-627-588
US-10-331-627-588
US-10-331-627-588
US-10-033-145-755 -09-955-518-18 Query Match Length Score 5 6 7 7 8 8 8 110 110 112 Result Š. U 0000

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Sequence 3, Application US/09953562; GENERAL INFORMATION: APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.

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RESULT 3 US-09-953-562-3/c

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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   Sequence 12, Application US/10371474

Sequence 12, Application US/10371474

Sequence 12, Application:

APPLICANT: Donna T. Ward

APPLICANT: William Gaarde

APPLICANT: Brett P. Wonia

APPLICANT: Jacqueline Wyatt

TILE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION

FILE REFERENCE: RFS-0169

CURRENT FILING DATE: 2008-02-21

PRIOR PLICATION NUMBER: US/09/676,436

PRIOR PLICATION NUMBER: US/09/676,436

PRIOR PLICATION NUMBER: US/09/676,436

PRIOR PLICATION NUMBER: US/09/676,436

SEQ ID NO 12

LENGTH: 20

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
FILE REFERENCE: RFS-0169
CURRENT APPLICATION NUMBER: US/10/371,474
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 89
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 20; 0.092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Antisense Oligonucleotide US-10-371-474-64
                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonuclectide US-10-371-474-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3314 AGGGATTCAGGGGTTCCAGC 3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64, Application US/10371474; GENERAL INFORMATION:
APPLICANT: Donna T. Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AGGGATTCAGGGGTTCCAGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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100.0%;
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3321 CAGGGGTTCCAGC 3333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          William Gaarde
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-371-474-64/c
US-10-371-474-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS TITLE OF INVENTION: CELL CARCINOMA
FILLE REFERENCE: E6114-01
CURRENT APPLICATION NUMBER: US/09/953,562
CURRENT FILING DATE: 2003-02-24
PRIOR PRIOR APPLICATION NUMBER: JP 2001-083352
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%; Score 12.4; DB 1; Length 14; 92.9%; Pred. No. 0.16; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      10496/P60122
                                                                                                                                         FILING DATE: 11-JAN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93111059,7
FILING DATE: 10-JUL-1993
PRIOR APPLICATION NUMBER: PCT/EP94/02218
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 6-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                            ; Sequence 24, Application US/09953562; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 61, Application US/10371474; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10490
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-9350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3314 AGGGATTCAGGGGTTC 3329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: homo sapiens
US-09-953-562-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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Best Local Similarity
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ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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US-09-953-562-24/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
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LENGTH: 24
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APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Rail-Hermann
APPLICANT: Schlingensiepen, Rail-Hermann
APPLICANT: Schlingensiepen, Rail-Hermann
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
NUMBER OF SEQUENCES: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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GENERAL INFORMATION:
APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
TITLE OF INVENTION: CELL CARCINOMA
FILE REFERENCE: E6114-01.
CURRENT APPLICANTON NUMBER: US/09/953,562
CURRENT FILING DATE: 2003-02-24
PRIOR PAPLICANTON NUMBER: JP 2001-083352
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 27
TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS TITLE OF INVENTION: CELL CARCINOMA FILE REFERENCE: E6114-01.

CURRENT APPLICATION NUMBER: US/09/953,562

CURRENT FILING DATE: 2003-02-24

PRIOR PALICATION NUMBER: JP 2001-083352

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.0%; Score 12.8; DB 1; Length 24; 87.5%; Pred. No. 0.13; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: FGFR3 mutagenic oligonucleotide US-09-953-562-3
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Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-591-486B-72; Sequence 72; Application US/08591486B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3314 AGGGATTCAGGGGTTC 3329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3314 AGGGATTCAGGGGTTC 3329
                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AGGGATGCAGGGGTAC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.55
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: homo sapiens
US-09-953-562-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                          SEQ ID NO 3
                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                       FEATURE:
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APPLICANT: Schlingensiepen, Georg F
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Karl Hermann
APPLICANT: Schlingensiepen, Karl Hermann
TITLE OF INVENTION: Wolfgang Brysch
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Tri
TITLE OF INVENTION: Of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OFFWARE: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) APPLICATION DATA:
                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Jacobson, Price, Holman & Stern: 400 Seventh Street, N.W. Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10496/P60122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 838-9350
TELERAX: (202) 393-9350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 13;
                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/591,486B FILING DATE: 11-74N-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93111059.7
FILING DATE: 10-JUL-1993
PRIOR APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 6-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
  400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 67, Application US/08591486B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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                                                                                                                       MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 83.3
Matches 10; Conservative
                    Washington, D.C
Y: U.S.A.
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                                                                                              COMPUTER READABLE FORM:
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US-08-591-486B-68
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                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Rail-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
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TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
TITLE OF INVENTION: CELL CARCINOMA
FILL REPERENCE: E0114-01
CURRENT APPLICATION NUMBER: US/09/953,562
CURRENT APPLICATION NUMBER: US/09.953,562
PRIOR APPLICATION NUMBER: J 2001-083352
PRIOR FILING DATE: 2001-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                      APPLICANT: William Gaarde
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Woatt
TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 10; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 3.7; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.0%; Score 9; DB 1; Length 29; Best Local Similarity 70.6%; Pred. No. 16;
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ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-10-371-474-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                  FILE REFERENCE: RTS-0169
CURRENT APPLICATION NUMBER: US/10/371,474
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US/09/676,436
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3315 GGGATTCAGGGGTTCCA 3331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
APPLICANT: Donna T. Ward APPLICANT: William Gaarde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3314 AGGGATTCAG 3323
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LENGTH: 20
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US-09-989-994-1270
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LENGTH: 10
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LENGTH: 10
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LENGTH: 10
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Patent No. US20020042138A1
GENERAL INFORMATION:
APPLICANT: TOWNES, Tim M.
APPLICANT: Donze, David
TITLE OF INVENTION: DELTA-ERTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: DELTA-ERTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 05118.0008U2
CURRENT APPLICATION NUMBER: US/09/955,518
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR FILMG DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.0%; Score 8.8; DB 1; Length 18; 83.3%; Pred. No. 15;
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0; Mismatches
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                                                        FILING DATE: 10-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 6-JUL-1994
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93111059.7
FILING DATE: 10-JUL-1993
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                                                                                                                                                             NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         TELEPAONE: (202) 638-6666
TELEFAX: (202) 393-9350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3314 AGGGATTCAGGGGTT 3328
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E: DNA (genomic)
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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MOLECULE TYPE: DN7
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US-09-953-562-26/c
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US-09-955-518-11
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LENGTH: 37
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TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS TITLE OF INVENTION: CELL CARCINOMA FILE REFERENCE: E6114-01 CURRENT APPLICATION NUMBER: US/09/953,562 CURRENT FILING DATE: 2003-02-24 PRIOR APPLICATION NUMBER: JP 2001-083352 PRIOR FILING DATE: 2001-03-22 NUMBER: OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: example target OTHER INFORMATION: DNA
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / 511-082
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
TATLE CANT: LIU, QIANE
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001.11-20
NUMBER OF SEQ ID NOS: 4085
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Pred. No. 18;
0; Mismatches 1; Indels
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: homo sapiens
US-09-953-562-26
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TYPE: DNA ORGANISM: Artificial Sequence
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90.0%;
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Matches 9; Conservative
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GENERAL INFORMATION:
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US-09-990-186-1337
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                                                                                                                                                          SEQ ID NO 1275
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                                                       Gaps
                                                                                                                                                                                                   Sequence 1337, Application US/09989994

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,994
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1337
LENGTH: 10
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TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: PRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / $11-US3
FILE REFERENCE: 8325-0011.21 / $11-US3
FURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001.11-20
NUMBER OF SEQ ID NOS: 4008
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO.1270
LENGTH: 10
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Pred. No. 18;
0; Mismatches 1; Indels
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                  Length 10;
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                      DB 1;
                      Score 8.4; DB Pred. No. 18; 0; Mismatches
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US-09-990-186-1270
; Sequence 1270, Application US/09990186
; GENERAL INFORMATION:
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90.0%;
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                      42.08;
90.08;
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                         Conservative
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ATGGATTCAG 10
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                                     Local Similarity
nes 9; Conserv
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US-09-990-186-1275
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SEQUENCE 1337, Application US/09990186

GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.21 / S11-US3
FILE REFERENCE: 8325-0011.21 / S11-US3
CURRENT APPLICATION UNMBER: US/09/990,186
CURRENT FILING DATE: 2001.11-20
NUMBER OF SEQ ID NOS: 4085
SEQ ID NO 1337
LENGTH: 10
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.21 / 811-US3
CURRENT APPLICATION NUMBER: US/09/990,186
CURRENT FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 18;
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Sequence 435, Application US/10330527
Sequence 435, Application US/10330527
Sequence 435, Application:
APPLICANT: Velculescu, Victor E.
APPLICANT: Valialer, Kenneth W.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 00107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 99/448,480
PRIOR FILING DATE: 1999-11-24
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Pred. No. 18;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 435
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TYPE: DNA
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                                                                                              42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 18; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                               Sequence 1496, Application US/10330627
GENERAL INFORMATION:
APPLICANT: Valculescu, Victor E.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Human Transcriptomes
FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 12002-12-30
PRIOR APPLICATION NUMBER: US 99/448,480
FRICK FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 90.0°
Matches 9; Conservative
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                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-435
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US-10-330-627-1496
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US-10-330-627-1546
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Matches 9; Conserv
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LENGTH: 10
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TRNGTH: 10
LENGTH: 10
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CHER INFORMATION: Description of Artificial Sequence: example target
CHER INFORMATION: DNA
US-09-989-789-1275
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                                  Sequence 1270, Application US/09989789

Patent No. US20020063379A1

GENERAL INFORMATION:
APPLICANT: LIU, Qiang

TITLE OF INVEWTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE

TITLE OF INVEWTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION 100.

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1270

LENGTH: 10
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APPLICANT: LIU, OLDAN
TITLE OF INVENTION:
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Patent No. US2020063379al
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
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Pred. No. 18;
0; Mismatches 1; Indels
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.vv
Best Local 9; Conservative
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Best Local Similarity 90.07
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US-09-989-789-1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHANKARA, SRINIVAS
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GAOZOLC
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT PILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PCT/US99/13800
PRIOR PILING DATE: 1995-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARE: Patentin Version 3.0
SEQ ID NO 524
LENGTH: 10
                                     ò.
  DB 1; Length 30;
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                                     3; Indels
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Pred. No. 30;
Mismatches
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40.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                        APPLICANT: Velculescu, Victor E.
APPLICANT: Vogelstein, Bert
TITE OF INVENTON: Human Transcriptomes
FILE REFERENCE: 001107,00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 588
  Score 8.2; DI
Pred. No. 43;
                                       0; Mismatches
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 524, Application US/10033145; Publication No. US20020151515A1; GENERAL INFORMATION: APPLICANT: GENYYME CORPORATION
                                                                                                                                                                                                                      Sequence 588, Application US/10330627 GENERAL INFORMATION:
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41.0%;
76.9%;
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Matches 8; Conservative
  Query Match
Best Local Similarity 76.93
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-330-627-588
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                                       Matches
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APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Gotingen, Wolfgang Brysch
TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatm
TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
NUMBER OF SEQUENCES: 185
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                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: example target ; OTHER INFORMATION: DNA US-09-989-789-1337
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SOFTWARE: PetentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: BAPPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNBER: EP 93111059.7
FILING DATE: 10-JUL-1993
PRIOR APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 10-JUL-1994
ATPONEY.FAGENT UNBER: 31,409
ATPONEY.FAGENT INFORMATION:
NAME: PLASEN INFORMATION:
TELEPHONE: (202) 6566
TELEPHONE: (202) 639-6666
TELEPHONE: (202) 639-6666
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 43:
SUDUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               Score 8.4; DB 1; Length 10;
Pred. No. 18;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Jacobson, Price, Holman & Stern: 400 Seventh Street, N.W.
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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            CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                   Query Match 42.0%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                           NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1337
LENGTH: 10
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US-08-591-486B-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-591-486B-43
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TITLE OF INVENTION: A Pharmaceutical Composition
TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Try
TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the
TITLE OF INVENTION: Treatment of Neoplasms
NUMBER OF SEQUENCES: 185
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SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,486B
FILING DATE: 11-JAN-1995
CLASSIFICATION: 514
PRICA PATENTIN DATA:
APPLICATION NUMBER: EP 93111059.7
FILING DATE: 10-JUL-1993
PRICA PAPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02218
FILING DATE: 6-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16;
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                                                                                                                                                                                                 Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh Street, N.W.
CITY: Washington, D.C
                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.0%; Score 7.8; DE Best Local Similarity 81.8%; Pred. No. 50; Matches 9; Conservative 0; Mismatches
                                                                                                              FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-17
                                                                                                                                                                                               40.0%; Score 8; DB ]
100.0%; Pred. No. 44;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schlingensiepen, Georg F
APPLICANT: Schlingensiepen, Relmar
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Gotingen, Wolfgang Brysch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10496/P60122 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 31
US-08-591-486B-163
Sequence 163, Application US/08591486B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Player, William E. REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 393-9350
TELEX: RC 24859 IDEA UR
INFORMATION FOR SEQ ID NO. 163:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
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                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: unknown
                                                                                                                                                                                                      Query Match 40.03
Best Local Similarity 100.
Matches 8; Conservative
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NUMBER OF SEQ ID NOS: 89
SEQ ID NO 17
LENGTH: 20
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ANTI-SENSE: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1337, Application US/10033145
; Sequence 1337, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
APPLICANT: GENEYME CORPORATION
APPLICANT: SHANKARA, SRINIVAS
; TILE OF INVENTION: PREPARATION AND USE OF SUBERIOR VACCINES
; TILE REFERENCE: GA02010.
CURRENT ELING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SEQ ID NO 1337
; SEQ ID NO 1337
; LENGTH: 10
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GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
FILE REFERENCE: RTS-0169
CURRENT APPLICATION NUMBER: US/10/371,474
CURRENT APPLICATION NUMBER: US/10/371,474
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                         APPLICANT: ROBERTS, BRUCE
APPLICANT: SHANKARA, SRINIVAS
TITLE OF INVENTION PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: GA0201C
CURRENT APPLICATION NUMBER: US/10/033,145
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: PGT/US99/13800
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 2137
SOFTWARR: Patentin version 3.0
SEQ ID NO 765
LENGTH: 10
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                    GENERAL INFORMATION:
APPLICANT: GENZYME CORPORATION
             Publication No. US20020151515A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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US-10-033-145-1337
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-033-145-765
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Best Local Similarity
Matches 8; Conserv
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TYPE: DNA ORGANISM: Artificial Sequence CRGANISM: Artificial Sequence: No. US20020042138Ale = CTHER INFORMATION: Synthetic construct US-09-955-518-18
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                                                                                                 RESULT 32
US-09-955-518-18/C
Sequence 18, Application US/09955518
Sequence 18, Application US/09955518
Sequence 18, Application US/09955518
GENERAL INFORMATION:
APPLICANT: TOWNES, Tim M.
APPLICANT: TOWNES, Tim M.
APPLICANT: DONZE, DAVId
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 05118-000802
CURRENT APPLICATION NUMBER: US/09/955,518
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

37.0%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.3e+04;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 2, 2003, 15:46:01 Job time : 3 secs
3314 AGGGATTCAGG 3324
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                      1 AGGGATAAAGG 11
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13, Appl 13, Appli 4, Appli 53, Appl 94, Appl 460, App 9, Appli 9, Appli

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Sequence 1
Sequence 4
Sequence 4
Sequence 5
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Sequence 4
Sequence 9
Sequence 9
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/07/704,288C
FILING DATE: A2-MAY-1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                  US-08-899-324-24
US-08-899-324-24
US-08-874-569B-13
US-09-955-518-13
US-09-955-518-4
US-09-955-518-4
US-09-508-753B-460
US-09-508-753B-94
US-09-508-753B-99
US-08-879-954-130
US-08-859-954-131
US-08-859-954-131
US-08-859-954-131
US-08-859-954-131
US-09-508-753B-289
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100.0%; Pred. No....
0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS:
TOPOLOGY: lin
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US-07-704-288C-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-07-704-288C-25/c
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Sequence 11, Appl
Sequence 123, App
Sequence 149, App
Sequence 21, Appl
Sequence 21, Appl
Sequence 239, Appl
Sequence 239, Appl
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253, App
6, Appli
6, Appli
18, Appl
18, Appli
5, Appli
5, Appli
5, Appli
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1023,400 Million cell updates/sec
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Sequence 22, A
Sequence 195,
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Sequence 172,
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                                                                                                                                                                time 0.001 Seconds
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-74-569B-11

US-09-508-753B-11

US-09-508-753B-149

US-09-508-753B-149

US-08-329-892B-21

US-08-899-324-21

US-08-899-954-239

US-08-590-804-239

US-09-508-753B-199

US-09-508-753B-199

US-09-958-18-18

US-08-329-892B-6

US-08-329-892B-6

US-09-508-753B-18

US-09-955-518-18

US-09-508-753B-121

US-09-608-753B-121

US-09-608-753B-121

US-09-608-753B-121

US-09-608-753B-121

US-09-608-753B-121

US-09-608-753B-121
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US-09-508-753B-22
US-09-508-753B-195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 50 summaries
                                                                                                                         - nucleic search, using sw model
                                                                                                                                                                    2, 2003, 15:40:42
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20
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Match Length
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length: 50
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Maximum DB seq
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Gaps

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3314 AGGGATTCAGGGGTT 3328
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                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                            Query Match 43.0%
Best Local Similarity 73.39
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: YUKO SHIBATA
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LENGTH: 37
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APPLICANT: Townes, Tim M.
APPLICANT: Donze, David
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 05118.0008U2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 10; DB 1; Length 10; 100.0%; Pred. No. 1.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                E: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                           TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/874,569B CURRENT FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P31 8899
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; Patent No. 6306650
                                                                                           Sequence 25, Application US/08379259
Patent No. 5695593
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                          California : United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
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10 AGGGGTTCCA 1
                                                                                                                                                                                                                                                                                                                                           Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                       RESULT 2
US-08-379-259-25/c
                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:\ No. 6306650e = OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: Biji OHARA
APPLICANT: Masanori MATAHTKI
TITLE OF INVENTION: Method for Synthesizing obna from mRNA sample
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TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 05118.0008U2
CURRENT APPLICATION NUMBER: 05/09955,518
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 37;
                                                                                                                                                                                                                                                                                                                           43.0%; Score 8.6; DB 1; Length 37; 73.3%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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Local Similarity 73.3%; Pred. No. 10;
nes 11; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEO ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 123, Application US/09508753B
; Patent No. 6544736
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PRIOR FILING DATE: 1997-09-18
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US-09-955-518-11/c
; Sequence 11, Application US/09955518
; Patent No. 6475740
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73.3%; Pic.
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APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REPERBNER: 1062/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: UP 9/270324
PRIOR APPLICATION NUMBER: UP 9/270324

PRIOR SEQ ID NOS: 472

SEQ ID NO 149

LENGTH: 10
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STREET: 3100 No. 5945329west Center, 90 S. 7th Street
CITY: Minneapolis
                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-149
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                                                                                                                                                                                        42.0%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 11; tive 0; Mismatches 1; Indels
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APPLICANT: Mortland-Brandt, Morten
APPLICANT: Mortensen, Uffe
APPLICANT: Olesen, Kjeld
APPLICANT: Stennicke, Henning
APPLICANT: Wagner, Fred
APPLICANT: Wagner, Fred
TITLE OF INVENTION: CUSTOMIZED PROTEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-508-753B-149/c
; Sequence 149, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: AXITA SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/08899324
Patent No. 5945329
GENERAL INFORMATION:
                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 90.09
                                                                                                                                                                                                               Best_Local Similarity 90.0
Matches 9; Conservative
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NUMBER OF SEQ ID NOS: 472
SEQ ID NO 123
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                                          LENGTH: 10
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ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6187579west Center, 90 S. 7th Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.0%; Score 8.2; DB 1; Length 30; 76.9%; Pred. No. 16;
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APPLICANT: Keilland-Brandt, Morten
APPLICANT: Keilland-Brandt, Morten
APPLICANT: Olesen, Vife
APPLICANT: Stennicke, Henning
APPLICANT: Fred
APPLICANT: Fred
APPLICANT: CONTENT ON CONTE
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                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,324
FILING DATE: 23-JUL-1997
CLASSIFFCATION: 435
PRIOR APPLICATION NUMBER: 08/229,892
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: 08/144,704
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: 08/144,704
FILING DATE: 28-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: KELIEBERGEY DENISE M
REGISTRATION NUMBER: 33,924
BREGISTRATION NUMBER: 33,924
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 86.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
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LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.99
Matches 10; Conservative
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COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
IMMEDIATE SOURCE:
CLONE: 0ligo N510
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US-08-329-892B-21
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INFORMATION FOR SEQ ID NO: 239: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 706-, TELEPHONE: 708-717-2430
TELEFAX: 713/651-5246
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LENGTH: 10 base,
TYPE: nucleic acid
                                                  LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                  3314 AGGGATTC 3321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Naperville
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                 ; ANTI-SENSE: YES
US-08-859-954-239
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TOPOLOGY: lir
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US-08-590-804-20
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Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%; Score 8.2; DB 1; Length 30; 76.9%; Pred. No. 16;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/859,954
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                                                                                                       NAME: Kettleberger, Denise M
REGISTRATION NUMBER:
REFERENCE/DCOKET NUMBER: 8648.44USO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-5900
                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/144,704
FILING DATE: 28-0CT-1993
ATTORNEY/AGENT INFORMATION:
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COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,714
                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 30 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
 FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3316 GGATTCAGGGGTT 3328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright
                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
CLONE: 01190 N510
                                                                                                                                                                                                                                                                                                                                    linear
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               CLASSIFICATION:
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US-08-859-954-239/c
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US-08-329-892B-21
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                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/08590804

Patent No. 5780273

GENERAL INFORMATION:

APPLICANT: Burg, J. Lawrence

TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE

TITLE OF INVENTION: NUCLEIC ACIDS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       DB 1; Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Data:
APPLICATION NUMBER: US/08/590,804
FILING DATE: 24-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION TOWNER: US/08/357,779
                                                                                                                                                                                                                    Query Match 40.0%; Score 8; DB 1; Lei
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 8; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Amoco Corporation
STREET: 55 Shuman Blvd., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/045,587 FILING DATE: 09-ARR-1993 ATTORNEY/AGENT INFORMATION: NAME: Galloway, No. 5780273val BREGISTRATION NUMBER: 33,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-899-324-6/c; Sequence 6, Application US/08899324; Patent No. 5945329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3100 No. 9 CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-899-324-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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US-08-329-892B-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 253, Application US/09508753B
Sequence 253, Application US/09508753B
Sequence 253, Application US/09508753B
Sequence 253, Application US/09508753B
Sequence 253, Application Waranion
APPLICANT: Akira SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATAHIKI
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Wethod for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 1997-09-18
FRIOR FILING DATE: 1997-09-18
WUMBER OF SEQ ID NOS: 472
SEQ ID NO 253
LENGTH: 10
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                                                                                                              US-09-508-753B-199

; Sequence 199, Application US/09508753B

; Patent No. 6544736
; Patent No. 6544736
; GENERAL INFORMATION:
    APPLICANT: Assulior FUNCIOLI
    APPLICANT: YAUGO SHIBATA
    APPLICANT: TURCO FUNAKI
    APPLICANT: HICOCO FUNAKI
    APPLICANT: Masanori WATAHIKI
    TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
    CURRENT APPLICATION NUMBER: US/09/508,753B
    CURRENT FILING DATE: 2000-06-16
    PRIOR APPLICATION NUMBER: US/09/508,753B
    NUMBER OF SEQ ID NOS: 472
    SEQ ID NOS: 472
    TEMPORE TO SECONO SE
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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3321 CAGGGGTT 3328
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                                    1 CAGGGGTT 8
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Best Local Similarity
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US-09-508-753B-253/c
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APPLICANT: Reilland-Brandt, Morten
APPLICANT: Keilland-Brandt, Morten
APPLICANT: Obesen, Kjeld
APPLICANT: Stennicke, Henning
APPLICANT: Stennicke, Henning
APPLICANT: Stennicke, Henning
APPLICANT: GUSTOWIZED PROTEASES
NUMBER OF SEQUENCES: 33
CORRESPONDENCES 33
CORRESPONDENCE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5945329west Center, 90 S. 7th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7.4; DB 1; Length 9; Pred. No. 4.5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SISTEM:
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,324
FILING DATE: 23-UUL-1997
CLASSIFICATION A15
PRIOR APPLICATION A15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/144,704
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: 08/144,704
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ketlaberger: Denise M
REGISTRATION NUMBER: 33,924
REGISTRATION NUMBER: 33,924
REGISTRATION NUMBER: 33,924
REGISTRATION NUMBER: 8648.44USC:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08329892B

Patent No. 6187579

GENERAL INFORMATION:

APPLICANT: Breddam, Klaus

APPLICANT: Keilland-Brandt, Morten
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
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0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                ; Sequence 18, Application US/09955518; Patent No. 6475740; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/07704288C; Patent No. 5399680; GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J. APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 444 COUNTY: LOS Angeles
CITY: LOS Angeles
STATE: California
COUNTY: United States
7TP: 9071-2921
                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3314 AGGGATTCA 3322
                                                                                                                                                                                                               3314 AGGGATTCA 3322
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Townes, Tim M. APPLICANT: Donze, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AGGGTTTCA 1
                                                                                                                                                                                                                                                  9 AGGGTTTCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-704-288C-5/c
                                                                                                                                                                                                                                                                                                                                US-09-955-518-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 18
LENGIH: 9
                                                                                                                                                                                                                                                                                                              RESULT 16
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                                                                                                                                 ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6187579west Center, 90 S. 7th Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DELTA-ERYTHROLD KRUPPEL-LIKE FACTORS AND TITLE OF INVENTION: METHODS OF USE FILE REFRENCE: 05118-000602-CURRENT APPLICATION NUMBER: US/08/874,569B CURRENT FILING DATE: 1997-06-13 PRIOR APPLICATION NUMBER: 60/019,769 PRIOR FILING DATE: 1996-06-14 SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7.4; DB 1; Length 9;
Pred. No. 4.5e+03;
0; Mismatches 1; Indels
                APPLICANT: Olesen, Kjeld
APPLICANT: Stennicke, Henning
APPLICANT: Wagner, Fred
TILE OF INVENTION: CUSTOMIZED PROTEASE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                Unskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,892B
FILING DATE: 27-CCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 8648.44US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08874569B; Patent No. 6306650; GENEAL INFORMATION: APPLICANT: Townes, Tim M. APPLICANT: Donze, David
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/144,704
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kettleberger, Denise M
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.0%;
88.9%;
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Mortensen, Uffe
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TELEFAX: 612/332-9081
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Best Local Similarity
                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-329-892B-6
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                                                                                                                                                                                             STATE: MN
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APPLICANT:
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; OTHER INFORMATION: Description of Artificial Sequence: No. 6306650e = ; OTHER INFORMATION: synthetic construct US-08-874-569B-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS

TOTALE OF INVENTION: ELEMENTS

CORRESPONDENCES: 26

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.0%; Score 7.4; DB 1; Length 9; 88.9%; Pred. No. 4.5e+03;
                                                                                                                             Query Match 37.0%; Score 7.4; DB 1; Length 9; Best Local Similarity 88.9%; Pred. No. 4.5e+03; Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
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Gaps

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APPLICANT: YUKO SHIBATA
APPLICANT: YUKO SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION WUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR PPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 87
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APPLICANT: Eiji OHARA
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
APPLICANT: Masanori WATAHIKI
APPLICANT: Masanori WATAHIKI
APPLICANT: Masanori WATAHIKI
APPLICANTON: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT PAPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-87
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Pred. No. 35;
0; Mismatches 1; Indels
                                                                Score 7.4; DB 1; Length 10;
Pred. No. 35;
                                                                                                            Indels
                                                                                                          7;
                                                                                                            0; Mismatches
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; Sequence 121, Application US/09508753B
; Patent No. 6544736
                                                                                                                                                                                                                                                                                                     Sequence 77, Application US/09508753B Patent No. 6544736; GENERAL INFORMATION:
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nilarity 88.9%;
Conservative (
; MOLECULE TYPE: DNA (genomic) US-08-379-259-5
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APPLICANT: ARITA SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: HIROKO FUNAKI
                                                                    37.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
                                                                       Query Match 37.0
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
ADDRESSEE: PRETITY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.4; DB Pred. No. 35; 0; Mismatches
                                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
             APPLICATION NUMBER: US/07/704,288C FILING DATE: 22-WAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/08379259; Patent No. 5695939
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                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown; MOLECULE TYPE: DNA (genomic)
US-07-704-288C-5
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 444 South Flower CITY: Los Angeles STATE: California COUNTRY: United States ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (619) 546-9392
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                                                                                                                                                                                                              TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 88.9
Matches 8; Conservative
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STRANDEDNESS: single
TOPOLOGY: unknown
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.asuhiro FURUICHI
APPLICANT: Hiroko FUNARI
APPLICANT: Hiroko FUNARI
APPLICANT: HAsanori WATAHIKI
TITLE OF INVENTION: Wethod for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT PILING DATE: 1097-09-18
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
LENGTH: 10
TYPE: P.
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hiroko FUNAKI
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

37.0%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 1; Indels
Ouery Match 37.0%; Score 7.4; DB 1; Length 10; Best Local Similarity 88.9%; Pred. No. 35; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.0%; Score 7.4; DB 1; Length 10; 88.9%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 134
LENGTH: 10
                                                                                                                                                                                                                         Sequence 134, Application US/09508753B Patent No. 6544736 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                 APPLICANT: AKITA SHIMAMOTO
APPLICANT: YASUHITO FURUICHI
APPLICANT: YUKO SHIBATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 88.9
Matches 8; Conservative
                                                                                 3317 GATTCAGGG 3325
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OTHER INFORMATION: Description of Artificial Sequence: Oligoribonucleotide
                                                                                                                                                APPLICANT: Hiroko FUNAKI
APPLICANT: E11 OHARA
APPLICANT: E11 OHARA
APPLICANT: Masanni WATAHIKI
TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT PAPLICATION NUMBER: US/09/508,753B
FILOR APPLICATION NUMBER: UP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 15
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Faul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
NUMBER OF SEQUENCES: 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.0%; Score 7.2; DB 1; Length 37; 75.0%; Pred. No. 54; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/859,954
                  Sequence 15, Application US/09508753B Patent No. 6544736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/08859954 Patent No. 6083695 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                        GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Paul, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3320 TCAGGGGTTCCA 3331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 75.0 Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aber:
STREET: Loc
Town Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 77010-3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
US-09-508-753B-15/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-508-753B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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US-08-859-954-292/C
Schence 292, Application US/08859954
Fatent No. 6083695
GENERAL INFORMATION:
FAPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Design and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
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                                 35.0%; Score 7; DB 1; Length 8; 100.0%; Pred. No. 5.1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUPTER READABLE PORM:

MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
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100.0%; Pred. No. ...
... 0; Mismatches
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TOPOLOGY: TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/632,782
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Patent No. 6109776
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.0 Best Local Similarity 100. Matches 7; Conservative
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TELEPHONE: 713/651-5246
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                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                             7 GGGATTC 1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
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US-08-859-954-292
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  US-08-859-954-240
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US-08-859-954-240/c
Sequence 240, Application US/08859954
Sequence 240, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Pred. No. 5.1e+03;
0; Mismatches 0; Indel.
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21P: 77010-3095

COMPUTER READABLE FORM:
MEDULU TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
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FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
REGISTRATION NUMBER: 32,714
REFERENCE/COCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5246
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
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APPLICATION NUMBER: 08/632,782
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100.0%; Pre
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INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
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Best Local Similarity 100.
Matches 7; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              3325 GGTTCCA 3331
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CLASSIFICATION:
                                                                                                                                                                                                                                                                  HYPOTHETICAL: YE
ANTI-SENSE: YES
US-08-859-954-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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                                                           FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-38
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Sequence 25, Application US/08590804
Patent No. 5780273
GENERAL INFORMATION:
APPLICANT: Burg, J. Lawrence
TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE
TITLE OF INVENTION: UNCLEIC ACIDS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/590,804
FILING DATE: 24-JAN-1996
CLASSIFICATION: 435
                                                                                                                                 Score 7; DB 1; Le
Pred. No. 5.1e+03;
0; Mismatches 0;
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. 56;
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100.0%; Pred. No. 56;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Amoco Corporation
STREET: 55 Shuman Blvd., Suite 600
CITY: Naperville
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/357,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US 08/045,587
FILING DATE: 09-APR-1993
ATONNEX/AGENT INFORMATION:
NAME: Galloway, No. 5780273val B
REGISTRATION NUMBER: 33,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32,468
                                                                                                                          35.0%; Scor
100.0%; Pre
0;
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TELECOMMUNICATION INFORMATION:
TELEPA: 708-717-2447
TELEFAX: 708-717-2430
             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                            Query Match 35.0 Best Local Similarity 100. Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                      RESULT 30
US-08-590-804-25/c
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US-08-590-804-25
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LENGIH: 8
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                     APPLICANT: Gene Logic, Inc.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Method and System for Computationally Identifying TITLE OF INVENTION: Clusters Within a Set of Sequences FILE REFERENCE: 77001.002

CURRENT APPLICATION WUMBER: US/09/063,450

CURRENT TILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO
                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:example; OTHER INFORMATION: sequence lilustrating a computational methodology US-09-063-450-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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; OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-398-499-15
                                                                                                                                                                                                                                                                                                                                                                                                                          0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09398499
Facent No. 6284466
GENERAL INFORMATION:
TILEORIE INFORMATION:
TILEOR INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REFERENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT FILING DATE: 1999-09-17
PRIOR FILING DATE: 1998-09-18
FILEORIE FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PATENTIN VOICE: 2.1
SEQ ID NO 15
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                  Length 8;
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APPLICANT: Benson, Andrew K.
TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
FILE REPERENCE: UNL 2963
CURRENT APPLICATION NUMBER: US/09/398,499
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/101,011
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.0%; Score 7; DB 1; Le Best Local Similarity 100.0%; Pred. No. 5.1e+03; Matches 7; Conservative 0; Mismatches 0;
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; Patent No. 6284466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Ver. 2.1
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      GENERAL INFORMATION:
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SEQ ID NO 38
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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| GGATTCA 7
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US-08-899-324-24/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yasuniro FURRICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hijo GHARA
APPLICANT: Hijo GHARA
TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
FILE REPERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
SEQ ID NOS: 472
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:Primer US-09-398-499-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10;
  Sequence 58, Application US/09398499

Sequence 58, Application US/09398499

Patent No. 6284466

GENERAL INFORMATION:

APPLICANT: Benson, Andrew K.

TILLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING

FILE REFERENCE: UNL 2963

CURRENT APPLICATION NUMBER: US/09/398,499

CURRENT APPLICATION NUMBER: 60/101,011

PRIOR FILING DATE: 1998-09-18

NUMBER FO FEQ ID NOS: 58

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 58

LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-508-753B-22/c; Sequence 22, Application US/09508753B; Patent No. 6544736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.1
Matches 7; Conservative
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APPLICANT: Akira SHIMAMOTO
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US-09-398-499-58
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US-09-508-753B-289/C
Sequence 289, Application US/09508753B
Fatent No. 6544736
GENERAL INPORMATION
APPLICANT: ARINA SHIMAMOTO
APPLICANT: TAUGH FURUICHI
APPLICANT: TAUGH FURUICHI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 289
LENTH: 10
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APPLICANT: Hiroko FUNAKI

APPLICANT: Biji OHARA

APPLICANT: Masanori WATAHIKI

TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample

FILE REFERENCE: 00162/HG

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT FILING DATE: 2000-16

PRIOR APPLICATION NUMBER: JP 9/270324

NUMBER OF SEQ ID NOS: 472

SEQ ID NO 195

LENGTH: 10

TYPE.
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Pred. No. 56;
0; Mismatches
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Keilland-Brandt, Morten
Mortensen, Uffe
Olesen, Kjeld
Stennicke, Henning
Wagner, Fred
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Patent No. 594529
GENERAL INFORMATION:
APPLICANT: Reilland-Brandt, Morten
APPLICANT: Nortensen, Uffe
APPLICANT: Olesen, Kjeld
APPLICANT: Stennicke, Henning
APPLICANT: Stennicke, Henning
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Best Local Similarity 100.0%; P:
Matches 7; Conservative 0;
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FEATURE: OTHER INFORMATION: Description of Artificial Sequence: No. 6306650e = OTHER INFORMATION: synthetic construct
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APPLICANT: DOORS, David
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE PACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REPRENCE: 05118.000802
CURRENT APPLICATION NUMBER: US/08/874,569B
CURRENT APPLICATION NUMBER: 05/019,769
PRIOR PRILING DATE: 1997-06-13
PRIOR PELLING DATE: 1997-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 37
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                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VETSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,892B
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION OF STATEMENT OF STATEMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 8648.44US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
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; Patent No. 6306650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Kettleberger, Denise M REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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LENGTH: 21 base pairs
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TELEFAX: 612/332-9081
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STRANDEDNESS: single
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CLONE: Oligo E145D
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          U.S.A.
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ORIGINAL SOURCE:
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          COUNTRY:
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                                                                                          E: Merchant, Gould, Smith, Edell, Welter & Schmidt 3100 No. 5945329west Center, 90 S. 7th Street
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TITLE OF INVENTION: CUSTOMIZED PROTEASES
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APPLICANT: Stennicke, Henning
APPLICANT: Wagner, Fred
TITLE OF INVENTION: CUSTOMIZED PROTEASE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8648.44USC1
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,324
FILING DATE: 23-UUL-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/329,892
FILING DATE: 27-00T-1994
APPLICATION NUMBER: 08/144,704
FILING DATE: 28-00T-1993
ATTORNEY/AGBUT INFORMATION:
NAME: Kettloberger, Denise M
REGISTRATION NUMBER: 33,924
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; Patent No. 6187579
; GENERAL INFORMATION:
APPLICANT: Breddam, Klaus
; APPLICANT: Keilland-Brandt, Morten
; APPLICANT: Mortensen, Uffe
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TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 24:
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MOLECULE TYPE: Genomic DNA
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TELEFAX: 612/332-9081
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LENGTH: 21 base pairs
TYPE: nucleic acid
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                              NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: Oligo E145D
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                                                                                                                                                          Minneapolis
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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US-08-329-892B-24/C
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GTTTCAGGAG 1
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US-09-508-753B-94
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APPLICANT: TOWNES, Tim M.
APPLICANT: Donze, David
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 05118.0008U2
CURRENT APPLICATION NUMBER: US/08/874,569B
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 49
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: TOWNES, Tim M.
APPLICANT: DOORS, David
FAPLICANT: DOORS, DALTA
FAPLICANT: DOORS, DALTA
FIRE PERENCE:
TITLE OF INVENTION: METHODS OF USE
FILE REPRENCE: 05118.000802
CURRENT APPLICATION NUMBER: US/09/955,518
CURRENT APPLICATION NUMBER: 06/019,769
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ FOR Windows Version 4.0
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Best Local Similarity 66.7%; Pred. No. 68;
Matches 10; Conservative 0; Mismatches
 Mismatches
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; Sequence 4, Application US/08874569B
; Patent No. 6306650
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US-09-955-518-13/c
; Sequence 13, Application US/0995518
; Patent No. 6475740
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                                       3314 AGGGATTCAGGGGTT 3328
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Matches 10; Conservative
   10; Conservative
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OTHER INFORMATION: Description of Artificial Sequence: No. 6475740e
OTHER INFORMATION: synthetic construct
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SERURAL INFORMATION:
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
SAPLICANT: Hiroko FUNAKI
APPLICANT: Hisoko FUNAKI
APPLICANT: Holara Masanori MATAHIKI
APPLICANT: Masanori MATAHIKI
TITLE OR INVENTION: Method for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
SEQ ID NO 53
LENGTH: 10
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Best Local Similarity 66.7'
Matches 10; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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Sequence 130, Application US/08859954 Patent No. 6083695
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Best Local Similarity 69.23
Matches 9; Conservative
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Matches 9; Conserva
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LENGIH: 21
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US-09-508-753B-460/C
Sequence 460, Application US/09508753B
Patent No. 6544736
Papticant: Vasuhiro FURUICHI
PAPLICANT: Vasuhiro FURUICHI
PAPLICANT: Wathory FUNATI
PAPLICANT: MATAHIKI
PAPLICANT: Matanori MATAHIKI
PAPLICANT: Method for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT FILING DATE: 2000-6-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 460
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                                     GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Fish OHARA
APPLICANT: Bish OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
FILE REFERENCE: 00162/HG
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34.0%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 2; Indels
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Sequence 94, Application US/09508753B Patent No. 6544736
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Best Local Similarity
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US-08-874-569B-9
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US-09-955-518-9
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GENERAL INFORMATION:
APPLICANT: TOwnes, Tim M.
APPLICANT: Townes, Tim M.
APPLICANT: Townes, Tim M.
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/019,769
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 21
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APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Pasign and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof
APPLICANT: Townes, Tim M.
APPLICANT: Donze, David
TITLE OF INVENTION: DELTA-ERYTHROID KRUPPEL-LIKE FACTORS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 05118.0008U3
CURRENT APPLICATION NUMBER: US/08/874,569B
CURRENT FILING DATE: 1997-06-13
PRIOR FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.0%; Score 6.6; DB 1; Length 21; 69.2%; Pred. No. 1e+02; tive 0; Mismatches 4; Indels
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TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
PRECFIPTION: /desc = "oligonucleotide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 270, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-5900
                                                                                                    NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REGISTRATION INBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-59
TELECOMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEPASX: 713/651-5246
                                                                                                                                                                              TELEPHONE: 713/651-5325
TELEPAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0%;
87.5%;
                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 87.5
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                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
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US-08-859-954-131
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Matches
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; Sequence 131 Application US/0885954
; Patent No. 6083655
; GENERAL INFORMATION:
APPLICANT: Hardin, Suan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STAMP.
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Wilbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-525
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us/08/859,954
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APPLICATION NUMBER: 08/632,782
FILING DATE:
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APPLICATION NUMBER: US
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM:
NUMBER OF SEQUENCES:
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                                                                                                              COUNTRY: U.S.A. ZIP: 77010-3095
                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE: YES US-08-859-954-130
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Gaps
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APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
Score 6.4; DB 1; Length 8; Pred. No. 5.1e+03; 0; Mismatches 1; Indels
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linear
8 TCAGGAGT 1
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CLASSIFICATION:
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STREET: 100.
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US-08-859-954-537
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                                                                     US-08-859-954-537/c
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                                                      RESULT 50
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APPLICANT: Hardin, Paul B.
APPLICANT: Hardin, Paul B.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6.4; DB 1; Length 8;
Pred. No. 5.1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                    Length 8;
                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                Query Match 32.0%; Score 6.4; DB 1;
Best Local Similarity 87.5%; Pred. No. 5.1e+03;
Matches 7; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D. 22,714
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
                                                                                                                                                                                                                                                                                                                                                   US-08-859-954-509/c; Sequence 509, Application US/08859954; Patent No. 6083695; GPNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
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INFORMATION FOR SEQ ID NO: 509:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
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87.5%;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 56
       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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CITY: Houston
STATE: Texas
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US-08-859-954-270
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                                                                       APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul B.
APPLICANT: Hardin, Paul B.
APPLICANT: Hardin, Paul B.
TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.0%; Score 6.4; DB 1; Length 8; 87.5%; Pred. No. 5.1e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: October 2, 2003, 15:40:43
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sequence 537, Application US/08859954 Patent No. 6083695 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.0 Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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TOIG Of: a42556
TOIG Of: a88747
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TOIG Of: ax62845
TOIG Of: ax62845
TOIG Of: ax62845
TOIG Of: ax62342
TOIG Of: ax62342
TOIG Of: ax62357
TOIG Of: ax62357
TOIG Of: ax62357
TOIG Of: ax62436
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TOIG Of: ax62570
TOIG Of: ax62627
TOIG Of: ax62627
TOIG Of: ax62627
TOIG Of: ax15252
TOIG Of: ax15358
TOIG Of: ax15358
TOIG Of: ax15358
TOIG Of: ax66782
TOIG Of: bd00320
TOIG Of: bd00320
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                                                      2003, 15:32:18; Search time 0.001 Seconds (without alignments) 17.800 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 42 summaries
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34	TOIG of: e39536 TOIG of: ar01795 TOIG of: ar30347 TOIG of: ar30367 TOIG of: ar30367 TOIG of: ar30367 TOIG of: ar30145 TOIG of: ar30154	linear PAT 06-MAR-1997	3	SCALINGERSIEPED, N. and 3 ANTISENSE-NUCLEIC ACID FOR L INJURY, DEGENERATION AND DPLASMS	Les Cont	N Check: 7525 Length 14; ; Indels 0; Gaps 0;		linear PAT 22-JAN-2000 WETHOD DE)
of: a8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	e39536 e54753 ar017955 ar303474 ar303528 ax301451 ax301542	14 bp	15 15	, Schlingensiepen, K., OMPOSITION COMPRISING TREATMENT OF NEURONAL THE TREATMENT OF NEO! A 72 19-0AN-1995, AU 7345694 950206.	="unidentified" ="genomic DNA" "taxon:32644" 3 g 4 t	2, 2003 14:56 Type: Score 12.4; DB 1; Pred. No. 2.3; 0; Mismatches 1	1 from: 1 to: 1	14 bp DNA Patent W09833904. 17 17 17 16 17 17 17 17 18 18 18 18 18 18
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AX628456.1 GI:28456494
AX471613
AX471613.1 GI:22206738
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                                   Homo sapiens (human)
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Schlingensiepen, K.H. and Brysch, W.
An antisense oligonelectide preparation method
Patent: JP 2001511000-A 895 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11,C07H21/04,A61K31/70
An antisense oligonucleotide preparation method FH
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JP 2001511000-A/895.
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07-AUG-2001
30-JAN-1998 JP 1998532533
31-JAN-1997 EP 97101531.
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; TOIG of: bd066260 check: 7525
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milarity 92.9%;
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Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           Hofmann, K., Conradt, M. and Petersohn, D. Method for determining skin stress or skin ageing in vitro Patent: Wo 02053773-A 1190 11-JUL-2002; HENKEL KGAA (DE) Location/Qualifiers
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55.0%; Score 11; DB 1;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 11; Conservative 0; Mismatches
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ax628456/c
; TOIG of: ax628456 check: 4620 from: 1 to: 11
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PAT 09-AUG-2002

linear

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                Hofmann,K., Conradt,M. and Petersohn,D.
Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 126 11-JUL-2002;
HENKEL KGAA (DE)
Location/Qualifiers
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Method for determining homeostasis of the skin
Patent: WO 02053774-8 469 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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90.9%; Pred. No. 10;
live 0; Mismatches 1
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AX470549 11 bp Dt
Sequence 126 from Patent WO02053773.
AX470549. GI:22205674
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                 PAT 04-APR-1998
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Zhu,Q. and Lamb,C.J.
Plant defense genes and plant defense regulatory elements
Patent: US 5695939-A 25 09-DEC-1997;
Location/Qualifiers
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184475
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Method for determining homeostasis of the skin
Petent: WO 0205374-A 3824 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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                    DNA
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8.9;
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; TOIG of: ax626783 check: 4483 from: 1 to: 11
              Sequence 25 from patent US 5695939. I84475.1 GI:3021995
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No.
Live 0; Mismatcl
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4 c 2 q
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Best Local Similarity 100.
Matches 10; Conservative
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Unclassified.
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Best Local Similarity
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PAT 21-FEB-2003

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining skin stress or skin ageing in vitro
Patent: WO 02053773-A 894 11-JUL-2002;
HENNEL KGAA (DE)
Location/Qualifiers
                                                                                                                                                                                          Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 10)
Hashimoto, S., Mateushima, K. and Suzuki, T. Genes with human dendritic cell expression Patent: JP 2000279181-A 299 10-OCT-2000; SCIENCE & TECH AGENCY
                                                                                                                                                                                                                                                                                                                                                                          PI SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC
C12N15/09, C07K14/475, C07K16/18, C12N15/00
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/organism='Homo sapiens (human)'.
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                                                        Genes with human dendritic cell expression. E39766
E39766.1 GI:18621857
JP 2000279181-A/299.
Homo sapiens (human)
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45.0%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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JP 2000279181-A/299
10-OCT-2000
01-APR-1999 JP 1999095481
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                                       TOIG of: e39766 check: 4052 from: 1
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ax471317
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 10;
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Method for determining homeostasis of the skin
Patent: WO 02053774-A 7890 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                      Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 6619 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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                             Score 9.4; DB 1;
Pred. No. 10;
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to: 11
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/organism="Homo sapiens"
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/db_rref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_txef="taxon:9606"
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Homo sapiens
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Best Local Similarity 90.9
Matches 10; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/mol_type="qenomic DNA"
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Sequence 2747 from Patent WO02053774.
AX625706 AX625706.1 GI:28453647
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/db_xref="taxon:9606"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method for determining homeostasis of the skin
Patent: WO 02053774-8 8823 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Patent: WO 02053774-A 3242 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
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Sequence 8823 from Patent WO020533774.
Ax631781 Ax631781 GI:28459888
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/cyganism="Homo sapiens"
/mol_type="genomic DNA"
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ilarity 100.0%; Pred. No. 12;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Shinmmoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and
Shimmamoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and Watahiki, M.
Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 123 08 APR-2003;
Location/Qualifiers
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Method for synthesizing cDNA from mRNA :
Patent: US 6544736-A 149 08 APR-2003;
Location/Qualifiers
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Sequence 12 from Patent W00127267.
AX112965.
AX112965.1 GI:13939400
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Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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manufacture of immunoregulatory compositions Patent: WO 0127267-7 12 19-APR-2001; ISIS INNOVATION LIMITED (GB)
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Patent: WO 0138577-435 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
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Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 17;
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Patent: WO 0138577-A 1546 31-MAY-2001;
The Johns Hopkins University (US)
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Patent: WO 0138577-A 1496 31-MAY-2001;
The Johns Hopkins University (US)
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_rref="taxon:9606" 3 g 2
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AX301326
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Pred. No. 17;
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Homo sapiens
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Best Local Similarity 90.0
Matches 9; Conservative
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\operatorname{Liu}_{\mathcal{O}}. Position dependent recognition of gnn nucleotide triplets by zinc
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Patent: WO 0242459-A 1337 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Patent: WO 0242459-A 1275 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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AX667888
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Pred. No. 17;
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Sequence 1275 from Patent WO0242459.
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AX667826.1 GI:29291363
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Pred. No. 17;
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Matches 9; Conserv
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                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0185941-A 40 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
Location/Qualifiers
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/wol_type="genomic DNA"
/db_xref="taxon:32630"
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ax667826
; TOIG of: ax667826 check: 3978 from: 1 to: 10
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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             Homo sapiens (human)
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90.0%;
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PAT 26-MAR-2003

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JP 2001327293-A/63
27-NOV-2001
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E 1 (bases 1 to 10)
S matsushima.K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
L Patent: JP 2001069993-A 38 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/38
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR ROJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
CILVALSO,COTK14/47,COTK16/18,GOIN33/50,GOIN33/53//A61K45/00, PC
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Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A,70 21-MAR-2001;
DAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PD 21-MAR-2001
PP 28-APR-2000 JP 2000131079
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/organism='Homo sapiens (human)'
Location/Qualifiers
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LPS activated human monocyte expressing genes.
BD007794 1 GI:18636167
JP 2001069993-A/70.
HOMO sapiens (human)
                                                 10 bp DNA line LPS activated human monocyte expressing genes. BD007762
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Pred. No. 17;
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; ToIG of: bd007794 check: 3919 from: 1 to: 10
                             to: 10
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    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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JP 2001069993-A/38.
Homo sapiens (human)
Homo sapiens
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RESULT 29
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22-MAY-2000 JP 2000150562
KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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1 (bases 1 to 10)

Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S. Human matured/activated dendritic cell expression genes Patent: JP 2001327293-A 63 27-NOV-2001;
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PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC
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    organism='Homo sapiens (human)'

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Pred. No. 17;
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; TOIG of: bd083142 check: 3920 from: 1 to: 10
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Hashimoto, S., Matsushima, K. and Suzuki, T. Genes With human dendritic cell expression
Patent: JP 2000279181-A 69 10-0cT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PI SHINICHI HASHIMOTO, KOJI MATSUSHIMA, TAKUJI SUZUKI PC C12N15/09, C07K14/475, C07K16/18, C12N15/00
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Genes With human dendritic cell expression.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OS Homo sapiens (human)
PN JP 2000279181-A/69
PD 10-OCT-2000
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JP 2000279181-A/69.
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Homo sapiens
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KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI, SHIGENORI PI
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                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10)
Matsushima, K., Hashimoto, S., Suzuki, T. and Nagai, S.
Human matured/activated dendritic cell expression genes
Patent: JP 201327293-A 125 27-Nov-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
PO HOMO Sapiens (human)
PD 20132793-A/125
PD 27-NOV-2001
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1 (bases 1 to 10)

Matsublima.K., Hashimoto,S., Suzuki,T. and Nagai,S.
Human matured/activated dendritic cell expression genes
Patent: 19 2001327293-A 189 27-NOV-2001;

OS Homo sapiens (human)

DY 201137293-A/189

PP 22-MAY-2001

PP 22-MAY-2001
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Human matured/activated dendritic cell expression genes.
BD083204
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Human matured/activated dendritic cell expression genes.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2001327293-A/189.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                     Unknown.
Unclassified.
1 (bases 1 to 10)
Shimamoto, A., Furuichi, Y., Shibata, Y., Funaki, H., Ohara, E. and
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Method for synthesizing cDNA from mRNA sample
Patent: US 6544736-A 253 08-APR-2003;
Location/Qualifiers
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Method for synthesizing cDNA from mRNA
Patent: US 6544736-A 199 08-APR-2003;
Location/Qualifiers
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; TOIG of: ar303528 check: 3871 from: 1 to: 10
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Sequence 253 from patent US 6544736.
AR303528 1GI:31692304
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Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches
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; TOIG of: ar303474 check: 3970 from: 1 to: 10
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Pred. No. 19;
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100.0%; Pred. No. ...
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Pred. No. 19; Mismatches
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Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
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Matches 8; Conservative
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Unclassified.
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Homo sapiens (human)

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 10)

Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.

Human normal liver cell expression genes

E Patent: JP 2001211883-A 105 07-AUG-2001;

SCIENCE & TECH AGENCY

OS Homo sapiens (human)

PN JP 2001211883-A/105

PD 07-AUG-2001

PF 31-JAN-2000 JP 2000023170

PP XOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
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                                                          PAT 27-AUG-2002
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Insertion elements and amplifiable nucleic acids
Patent: US 5780273-A 20 14-JUL-1998;
Location/Qualifiers
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                                                Human normal liver cell expression genes. E54753 GI:22556236 JP 2001211883-A/105.
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Pred. No. 17;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_tref="taxon:9606"
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Sequence 20 from patent US 5780273.
AR017955
AR017955.1 GI:3973558
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  RESULT 35
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PAT 15-APR-2003
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0185941-A 256 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
Location/Qualifiers
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Patent: EP 1295950-A 20 26-MAR-2003;
GT Diagnostics B.V. (NL)
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Sequence 20 from Patent EP1295950.
AX719148
           Pred. No. 19;
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Matches 8; Conservative 0; Mismatches
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0185941-A 165 15-NOV-2001;
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
Location/Qualifiers
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Patent: WO 0138577-8 588 31-MAY-2001;
The Johns Hopkins University (US)
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Sequence 165 from Patent WO0185941.
AX301451
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? a 1 c 4 g 3
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Sequence 588 from Patent WO0138577.
AX152673 GI:14534324
AX152673.1 GI:14534324
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ilarity 100.0%; Pred. No. 19;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3315 GGGATTCA 3322 .

Qy 3315 GGGATTCA 10

Search completed: October 2, 2003, 15:32:19
Job time: 1 secs
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34 8.4 42.0 10 1 aah63595 7 1015 05:35 8.4 42.0 10 1 aah64556 7 1015 05:35 8.4 42.0 10 1 aah64706 7 1015 05:39 8.4 42.0 10 1 aas167389 7 1015 05:39 8.4 42.0 10 1 aas167389 7 1015 05:40 8.4 42.0 10 1 aas37315 7 1015 05:40 8.4 42.0 10 1 aav35904 7 1015 05:40 8.4 42.0 10 1 aav36904 7 1015 05:40 8.4 42.0 10 1 aav36906 8.4 42.0 10 1 aav36904 7 1015 05:40 8.	8.4 42.0 10 1 aa284309		74 8 40.0 10 1 aaz832571 7015 0517 75 8 40.0 10 1 aaz84157 7016 0517 75 8 40.0 10 1 aaz84157 7016 0517 77 8 40.0 10 1 aaz84157 7016 0517 77 8 40.0 10 1 aaz84157 7016 0518 8 40.0 10 1 aaz84401 7016 0518 8 40.0 10 1 aaz845236 7016 0518 8 40.0 10 1 aaz85536 7016 0518 8 40.0 10 1 aaz85536 7016 0518 8 40.0 10 1 abk14551 7016 0518 8 40.0 10 1 abk23538 7016 0518 8 40.0 10 1 abk23538 7016 0518 8 40.0 10 1 abk35539 7016 0518 8 40.0 10 1 abk35539 7016 0518 8 40.0 10 1 abk35539 7016 0518 8 8 40.0 10 1 abk35539 7016 0518 8 8 40.0 10 1 abk3539 7016 0518 8 8 40.0 10 1 abk3539 7016 0518 8 40.0 10 1 abk3559 7016 0518 8 40.0 10 1 abk3559 7016 0518 8 40.0 10 1 abk3559 7016 0518 8 40.0 10 1 abk353985.
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. nucleic search, using sw model October 2, 2003, 15:35:57 ; Search time 0.001 Seconds 36.640 Million cell updates/sec	676-436-3 attcaggggttccagc 20 TY_NUC 10.0 , Gapext 0.5 s, 916 residues atisfying chosen parameters: 178	Match 0% Match 100% first 89 summaries * Imber of results predicted by chance to have sor equal to the score of the result being prinalysis of the total score distribution. SUMMARIES gth DB ID Description	100.0 20 1 aad37150

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The present invention relates to antisense compounds, compositions and methods for modulating the expression of MEKK4 (also referred as mitogenactivated protein kinase kinase 4; MAPIK4; MAP three kinase 1; MAP/ERK kinase kinase 4; MAPKK4; MTK1). The antisense oligos are useful for inhibiting the expression of MEKK4 in cells or tissues. They are also useful for treating an animal having a disease or condition associated with MEKK4 such as immunological, inflammatory, hyperprollferative
Human; MEKK4 modulation; mitogen-activated protein kinase kinase 4; MTK1; MAP3K4; MAP three kinase 1; MAP/ERK kinase kinase 4; MAPKKK4; cytostatic; prophylaxis; immunological; hyperproliferative disorder; cancer; therapy; antisense; inflammatory; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense compound targeted to nucleic acid encoding mitogen-activated protein kinase 4, useful for treating immunologic disorder, inflammatory disorder or cancer
                                                                                                                                                                                /mod_base= OTHER
/note= "2'-methoxyethyl nucleotides"
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/note= "Phosphorothioate backbone"
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/mod_base= OTHER
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Antisense nucleic acid hybridising with an area of the mRNA and/or DNA comprising the genes c-jub, jun-B or c-fos, expression of which plays a causal role in neuronal injury, degeneration, cell death and/or neoplasms, can be used to prevent and treat such conditions. c-jun antisense sequences are described in AAQ83267-321 and AAQ8344-45; and c-fos antisense sequences are described in AAQ83364-439 and AAQ83446-51. Preferably the antisense sequences are pescribed in AAQ8346-51 and c-fos antisense sequences are described in AAQ8346-51 preferably the antisense sequences are phosphorothioate oligonucleotides since these are not destroyed as fast by endogenous
disorder or cancer. Sequences of the invention are also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. They are also useful in antisense therapy. The present sequence is an antisense oligonucleotide targetted to human MEXK4 DNA. This sequence is used in the exemplification of the invention.
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Matches 20; Conserv
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20-SEP-1995
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aaq83338
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aaq83338

RESULT 3 abq87435/c

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; socacea, metalonam; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                             Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Pred. No. 9.6;
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aaz83859/c
; TOIG of: aaz83859 check: 3883 from: 1
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                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-2001; 2001WO-EP15179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2001; 2001DE-1000127.
                                                                       ABV67711 standard; cDNA; 11
                                 TOIG of: abv67711 check: 4620
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                                                                                                                                                                                       Human skin KST 5497.
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                             WO200253774-A2.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                   21-OCT-2002
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                                                                                                               ABV67711;
RESULT 4
abv67711/c
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                                                                         q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying genes involved in skin stress and ageing, useful e.g. in screening for cosmetic or therapeutic agents, based on differential
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Human skin stress/ageing related EST &EQ ID NO 1190.
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                                       DB 1;
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9.6;
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                                                     Pred. No. 4.2;
0; Mismatches
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                                       Score 12.4;
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Pred. No.
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                                   62.0%;
92.9%;
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                                                                                                               3318 ATTCAGGGGTTCCA 3331
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                                                                                                                                       1 ATTCAGGCGTTCCA 14
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                                                                             Conservative
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es 11; Conserv
                                                       Best Local Similarity
Matches 13; Conserv
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Best_Loc Matches

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Length 11; Indels 11

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                                                    ABV66038 standard; cDNA; 11
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abv66038/c
7 TOIG of: abv66038 check: 4483
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                                                                                                                           21-OCT-2002 (first entry)
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast transcribts tumour tissue (i.e. are upregulated in metastatic breast transcribts).

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification caretions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected call types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising useful in vaccines; for diagnosing breast cancer and for raising to expend and isolate populations of educated, antigen-specific immune ceffecter cells, e.g. cytotoxic T lymphocytes, and these used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer
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                                                                          Human; metastatic breast tumour tissue; breast cancer; tag; primer;
                                     Metastatic breast tumour cell upregulated transcript tag #3093
                                                                                       non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                                                               98US-0089853.
98US-0089997.
98US-0090039.
98US-0090040.
                                                                                                                                                                                                                                                                99WO-US13647
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ROBERTS B L.
SHANKARA S.
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                                                                                                                                                                                   WO9965928-A2
                                                                                                                                                                                                                                                                                                                                      19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts BL,
                                                                                                                                                                                                                                                              18-JUN-1999;
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(GENZ) (ROBEZ) (SHANZ)

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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus: rosacea; melanoma; basid cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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100.0%; Pred. No. 14;
iive 0; Mismatches (
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aa142209/c
; TOIG of: aa142209 check: 4662 from: 1 to: 11
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Query Match

Matches

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RESULT 9
abv62683/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a method of screening for antibiotic agents. The method involves disrupting binding of the 5' and 3' hinge regions of method involves disrupting binding of the 5' and 3' hinge regions of the arbosomal RNA precursor (pre-rRNA) thereby preventing processing of the ribosomal RNA precursor (pre-rRNA). Thereby preventing processing of translation machinery. The method of the invention is useful in screening for antibiotics which can be used to inhibit cell growth of infectious organisms and/or treat opportunistic infections in eukaryotic hosts (i.e. bumans and domestic animals). The antibiotics identified by the method of the invention may be used to treat opportunistic infections in humans (e.g. fungi, protozoa and multicelular parasites, chagas disease caused by Trypanosoma cruzi, and Pneumocystis carinii infections in immunocompromised hosts). The antibodies identified by the method of the immunocompromised hosts). The antibodies identified by the method of the immunocompromised hosts). The antibodies in domesticated animals (e.g. coccidiosis in poultry caused by infection with Eimeria). The present RNA sequence represents the Saccharomyces cerevisiae U3 snoRNA 3'
             Saccharomyces cerevisiae U3 small nucleolar RNA (snoRNA) 3' hinge region.
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                                                                                                                                                                                                                                                                                                                                                     Identification of antibiotic agents, useful to treat opportunist
infections in humans and domestic animals, comprises disrupting binding
of specific regions of U3 small nucleolar ribonucleic acid to
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                                      U3 snoRNA 3' hinge region; ss; antibiotic agent screening; yeast; U3 small nucleolar RNA domain I hinge region; snoRNA; pre-rRNA; 18S rRNA subunit; cell growth inhibition; fungal infection; protozoa infection; chagas disease; frypanosoma cruzi infection; Pneumocystis carinii infection; coccidiosis; Eimeria infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      October 2, 2003 14:57 Type: N Check: 4662
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                complementary sequences in pre-rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 18; 74pp; English.
                                                                                                                                                                                                                                                                                                 Lange TS;
                                                                                                                                                                                                                                                                     (UYBR-) UNIV BROWN RES FOUND.
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                                                                                                                                                                                                              28-JUN-2001; 2001WO-US20520
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90.9%;
                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                 Borovjagin A,
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Matches
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The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; and identifying or determining the effects of skin ageing and/or stress; and identifying or determining the effects of sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying genes involved in skin stress and ageing, useful e.g. in screening for cosmetic or therapeutic agents, based on differential
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                                                         Human; skin ageing; skin stress; EST; expressed sequence
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Human skin stress/ageing related EST SEQ ID NO 126
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Best Local Similarity 90.9%;
Matches 10; Conservative
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Hofmann K;

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Conradt M,
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                   WPI; 2002-590638/63
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                                                               e.g. skin cancer
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Petersohn D,
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the stand of the present sequence is that of a human expressed sequence tag
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                                                                                                                                  In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 18;
0; Mismatches 1
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                                                                                                                                                                              Disclosure; Page 38; 1345pp; German.
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                         20-DEC-2001; 2001WO-EP15179.
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                                           03-JAN-2001; 2001DE-1000127
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                        Conradt
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                                                                                                              WPI; 2002-590638/63.
                                                                   (HENK ) HENKEL KGAA
                                                                                                                                                         e.g. skin cancer
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                                                                                        Petersohn D,
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   11-JUL-2002.
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. ($AGE$) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; icosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 18;
0; Mismatches 1; Indels
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                                                                                                                                                           Disclosure; Page 209; 1345pp; German.
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90.9%;
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21-DEC-2000
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                                                                                              The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (ESI) of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Page 251; 1345pp; German.
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Local Similarity 90.9%;
nes 10; Conservative
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lesser ext
           Claim 24;
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Matches
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coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at phase, 5 phase and 62/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a system cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which expression of the yeast gene is a candidate antifungal drug; (3) a method
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SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114 to AAC74213), each is continuous with the base sequence 5'-CATG-3' located most closely to the poly-A region. The sequences can be used for the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study an diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers and autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerevisiae; characterisation; cell cycle; NORF;
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100.0%; Pred. No. 24;
rative 0; Mismatches
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of gene expression (SAGE) tags, useful
affecting phases of the cell cycle -
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Best Local Similarity 100..
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progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in MI; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell of at least NORF gene whose expression is affected by the class of drugs. The NORF consequence of the class of drugs in the yeast cell of at least consequence may be used to study, monitor and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs.

ARF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present
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psychological disorder; single nucleotide polymorphism; alcoholism;
antiarteriosclerotic; anorectic; PCR; primer extension oligonucleotide;
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches
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AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while
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atherosclerosis, obesity, psychological disorders and alcoholism. The present sequence is an allele specific primer extension oligonucleotide used to isolate the human NPY coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                                                                                                                                      Gaps
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                                                                                            Check: 3815
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                                                                                                                                        Length 10;
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                                                                                                                                        DB 1;
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Pred. No.
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                                                               Sequence 10 BP; 2 A; 5 C; 1 G;
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98US-0089997.
98US-0090039.
98US-0090040.
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Best Local Similarity
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promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for
                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                         AAZ83465 Length: 10 October 2, 2003 14:57 Type: N Check: 3729
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                                                                                                                                   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 other;
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                                                                                                                                                                                          45.0%; Score 9; DB 1;
100.0%; Pred. No. 24;
tive 0; Mismatches
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98US-0090039.
98US-0090040.
98US-0090041.
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                                                                                                           adoptive immunotherapy.
                                                                                                                                                                                                                   Conservative
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Best Local Similarity
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19-JUN-1998;
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that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, prognosis, prognosis, prognosis, prognosis, preactions to preact cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense cell types, of e.g. therapeutic genes (also ribozymes or antisense cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; B-factor; properdin; BF; primer; ss; gene therapy; drug screening; antidiabetic; dermatological; diabetes; immunosuppressive; antiinflammatory; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to single nucleotide polymorphisms in the gene
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Best Local Similarity
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RESULT 19
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cof the copies of the gene is defined by one of the Br haplotypes given in the specification or whether both copies are defined by a haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair. This method is useful in genotypes. An association between a trait and comparing the frequency of the Br gene can be identified by comparing the frequency of the haplotype pair in a comparing the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype or haplotype pair in a reference population indicates the trait is associated with the thaplotype or haplotype pair. Be and its corresponding DNA are used for studying the expression and function of BF, for use in screening for candidate drugs to treat diseases related to BF activity, such as diabetes and systemic lupus erythematosus. Sequences ABK64105
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/standard_name= "exon binding site 1"
/note= "binds to bases 25-26 of sequence in
AAF30843"
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/standard_name= "delta"
/note= "binds to bases 31-32 of sequence in
AAF30843"
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/standard_name= "delta"
/note= "binds to base 34 of sequence in
AAF30843"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               AAF30844;
                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                            RESULT 18
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The present sequence is that of the exon binding site 1 (EBSI)
and delta region element of a group II intron sequence selected to
specifically base pair with a target region (see AAF30843) within
the human CCRS chemokine receptor gene. The target region was
tdentified in a screening of CCRS DNA for sequences matching the
wild-type DNA target site (see AAF30827) of the 1.1.trB group II
wild-type DNA target site (see AAF30827) of the 1.1.trB group II
intron (see AAF30828) of Lactococcus lactis. The intron,
designated CCRS-435s (435s indicating the insertion site on the
sense strand of the CCRS gene) and also including an EBS2 site
(5'GUGACG) was identified following cloning of the target sequence
into a recipient vector and selecting introns from a combinatorial
library having randomised target site recognition sequences (EBS
and delte). The selected intron CCRS-435s demonstrated a targeting
induction. Other selected introns were demonstrated to function in
human cells. This is an example of the selection of group II introns
thuman cells. This is an example of the selection of group II introns
thuman cells. This is an example of the selection of group II introns
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thuman cells. This is an example of the selection of group II introns
thus specifically integrate into specific DNA target sites. In the
the specifically infection and AIDS progression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel construct comprising a modified group II intron sequence comprising modified EBS1, EBS2 or delta sequence, or partially deleted loop sequence in domain IV, and promoter for regulating intron transcription -
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100.0%; Pred. No. 22;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Karberg M;
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13-OCT-2000; 2000US-0159724.
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Best Local Similarity 100.
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WO200129059-A1.
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                                                                            26-APR-2001
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis or determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacca; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                In vitro identification of skin-expressed genes, useful for determining
                                                                                                                                      homeostasis and identifying cosmetic or pharmaceutical agents against
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                      Hofmann K;
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100.0%; Pre
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                      Conradt M,
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9; Conservative
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                                                                WPI; 2002-590638/63.
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                                                                                                                                                                 e.g. skin cancer
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                      Petersohn D,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention.
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                                                                                                                                                                                                                                                                                                                                      Identifying genes involved in skin stress and ageing, useful e.g. in screening for cosmetic or therapeutic agents, based on differential
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; TOIG of: abv63615 check: 4819
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9; Conserve
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer
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RESULT 21
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                                 The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically senced factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (MI) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis; anner; sebornhea; lupus ertythematosus; rosaces; melanoma; basal cell carcinoma and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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to:
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               Disclosure; Page 100; 1345pp; German.
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; TOIG of: abv64961 check: 4510 from: 1
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                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                           e.g. skin cancer
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Best Local Similarity
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disorders, specifically neurodermatitis; sunburn, psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.
determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; soleroderma; loththyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention.
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abv65456
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3325 GGTTCCAGC 3333
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Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 other;
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                                                           45.0%; Score 9; DB 1; 100.0%; Pred. No. 22;
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100.0%; Pred. No. 22;
Live 0; Mismatches
                                                                      Pred. No. 22;
0; Mismatches
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abv71036
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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abv71036
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The present invention describes 100 human genes, which are expressed most frequently in human monocytes. The cDNA of each gene has a sequence fully defined in the specification, and lacking the CATG sequence located adjacent to polyA region, and lacking the CATG (1) an antibody specifically for the protein encoded by any of the genes; (2) oligonucleotides obtained from the cDNA sequences; (3) 380 human genes which are expressed most frequently in human macrophages, differentiated from human monocytes by granulocyte-macrophage colony-stimulating factor, the cDNA of each gene as fully defined sequence, given in the specification, lacking the base sequence CATG located most closely to the poly A region; (4) an antibody specifically for the protein encoded by any of the genes of (3); and (5) oligonucleotides obtained from the cDNA sequences of (3); and cDNAs, are used for the study of gene specificity and disease onset mechanism e.g. oncogenesis, genetic diseases, drug development and diagnosis. AAA56107 to AAA56586 represent specifically
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                                                                                                                                                                                                                                                                                                                                                                                         Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag; granulocyte-macrophage colony-stimulating factor; characterisation; GM-CSF; identification; diagnosis; gene specificity; oncogenesis; disease onset mechanism; genetic disease; drug development; ss.
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                                                                                                                                                                                                                                                                                                                Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:28
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to: 10
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    TOIG of: aaa56134 check: 3920 from: 1
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                                                                                 BP.
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(1) an antibody specifically for the protein encoded by any of the genes; (2) oligonucleotides obtained from the CDNA sequences;

(3) 380 human genes which are expressed most frequently in human macrophages, differentiated from human monocytes by granulocyte-macrophage colony-stimulating factor, the CDNA of each gene as fully defined sequence, given in the specification, lacking the base sequence CATG located most closely to the poly A region;

(4) an antibody specifically for the protein encoded by any of the genes of (3); and (5) oligonucleotides obtained from the CDNA sequences of (3). The genes and cDNAS, are used for the study of gene specificity and disease onset mechanism e.g. oncogenesis, genetic diseases, drug development and diagnosis. AAA56107 to AAA56586 represent specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes most frequently expressed in human monocytes and GM-macrophages and M-macrophages studied and with cDNAs characterized, for study of gene specificity, disease onset mechanism, drug development and
                                                                                                                                                                                                                     Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag; granulLocyte-macrophage colony·stimulating factor; oharacterisation; GM-CSF; identification; diagnosis; gene specificity; oncogenesis; disease onset mechanism; genetic disease; drug development; ss.
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                                                                                                                                                                                             Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:183
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    3322 AGGGGTTCCA 3331
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                                                                                                                                             AAA56289;
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                                                                    RESULT 26
                                                                              aaa56289
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The present invention describes 100 human genes, which are expressed most frequently in human monocytes. The CDNA of each gene has a sequence fully defined in the specification, and lacking the CATG sequence located adjacent to polyA region. Also described are:

(1) an antibody specifically for the protein encoded by any of the genes; (2) oligonuclectides obtained from the CDNA sequences;

(3) 380 human genes which are expressed most frequently in human macrophages, differentiated from human monocytes by any of the part as a fully defined sequence, given in the specification, lacking the has a fully defined sequence, given in the specification, lacking the has sequence CATG located most closely to the poly A region;

(4) an antibody specifically for the protein encoded by any of the genes of (3); and (5) oligonucleotides obtained from the CDNA sequences of (3). The genes and CDNAs, are used for the study of gene specificity and disease onset mechanism e.g. oncogenesis, genetic diseases, drug development and diagnosis. AAAS6107 to AAA56586 represent specifically contained oligonucleotide tag sequences for human genes expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes most frequently expressed in human monocytes and GM-macrophages and M-macrophages studied and with cDNAs characterized, for study of gene specificity, disease onset mechanism, drug development and
                                                                                                                                                                                                                                                                                                                                                 Human; monocyte; macrophage; GW-macrophage; W-macrophage; tag; granulocyte-macrophage colony-stimulating factor; obaracterisation; GW-CSF; identification; diagnosis; gene specificity; oncogenesis; disease onset mechanism; genetic disease; drug development; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                              Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:285.
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to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suzuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISC-) JAPAN SCI & TECHNOLOGY CORP.
check: 3920 from: 1
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                                                                  AAA56391 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsushima K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0307532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-JP05982
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                                                                                                                                                                                                               07-SEP-2000 (first entry)
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Matches 9; Conservative
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TOIG of: aaa56391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                            AAA56391;
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                                        The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells; a group of genes which are expressed at a higher frequency in human dendritic cells than in human monocytes; and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Each group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:11 to 100 (AAC74014 to AAC74013), SEQ ID NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74213), each is continuous with the base sequence be used for the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of
                                                                                                                                                                                                                                                          monocyte; immune system; diagnosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC73982 Length: 10 October 2, 2003 14:57 Type: N Check: 3920
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                                                                                                                                                                                                                                Human dendritic cell cDNA base sequence oligonucleotide #69.
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                                                                                                                  to: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. cancers and autoimmune diseases.
                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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                                                                                                                                              AAC73982 standard; cDNA; 10 BP.
                                                                                                                                                                                                                                                                           autoimmune disease; tumour; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease and tumors
                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2000; 2000WO-JP02019.
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                                                                                                                  TOIG of: aac73982 check: 3920
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90.0%;
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                                                                                                                                                                                                                                                             Human; dendritic cell;
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                3322 AGGGGTTCCA 3331
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                                           1 AGGCTTCCA 10
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                                                                                                                                                                                                                                                                                                                                   WO200060074-A1.
                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                         AAC73982
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Best Local 8
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                                                                                    RESULT 28
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and 62/M: (3) a method (M2) for screening candidate antifungal drug comprising: (a) contacting a test substance with a cycle expression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contecting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies at least 10 contiguous nucleotides of a NORF gene whose expression varies at land (4) a method (M4) for identifying a candidate drug as a method (M4) for identifying a candidate drug as a candidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in a drifect phases of the cell cycle. The methods m
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the present invention. AAF33262 to AAF33267 represent linkers and PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nor previously assigned open reading frame; nonamortated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
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     to: 10
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of gene expression (SAGE) tags, useful
affecting phases of the cell cycle -
TOIG of: aaf36987 check: 3940 from: 1
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                                                                                                       AAF36987 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                     23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-1999;
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invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising admiristering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose cypression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which most in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a comprising contacting a yeast cell with a cast in M1; and 40 and a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs.

AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33267 represent linkers and PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
                                                                                                                                                                                                                                                                              nor previously assigned open reading frame; nonamnotated ORF; SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
           Gaps
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                                                                                                                                                                                                                                                       Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6469.
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d. No. 30;
Mismatches
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Pred.
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                                                                                                                                                                                                                              (first entry)
ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
                                         3314 AGGGATTCAG 3323
                                                                      AAGGATTCAG 10
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Best Local Similarity
Matches 9; Conserv
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamnotated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a cycle cyclession varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (CC (M3) for identifying human genes which are involved in cell cycle expression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies cas in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene
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primers used in the SAGE method, in the exemplification of the present
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                                                                                                                                                                 Check: 3916
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                                                                                                                                                                                                                                                               Score 8.4; DB·1; Length 10;
Pred. No. 30;
); Mismatches 1; Indels
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                                                                                                                                                                    October 2, 2003 14:57 Type: N
                                                                                                     Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;
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Best Local Similarity 90.0
Matches 9; Conservative
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aaf39730
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expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs.

AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated genes differentially expressed in T helper 1 (Th1) and 2 (Th2) and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis and therapy of inflammatory and immune diseases.
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90.0%;
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The present invention describes an isolated gene (I) obtainable by:

(a) comparing the expression of one or more genes in populations of T helper I lymphocytes (ThI). Th2- and T regulatory cells (Treg)-enriched cell populations to identify a gene which is differentially expressed in antidiamentory, immunosuppressive, antiarteriosclerotic, antiallerior, antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer activities. (I) can be used in anti-inflammatory and immunoregulatory compositions for use in therapy, prophylaxis, or diagnosis and/or in a planamaceutical excipient, a unit dosage form or in a form suitable for local or systemic administration. Methods from the present invention can be used for detecting Th1 and/or Treg cells in a biological sample, for cell typing or for determining the number of Th1 and/or Treg and/or Treg cells in a biological sample. Diseases which may be treated by compositions of the invention include rheumatoid and osteoarthritis, diabetes, inflammatory bowel diseases, vascular diseases e.g. atherosclerosis and vasculitis, skin diseases such as psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus silerosis, and lung diseases e.g. chronic bronchtis, emphysema, conserved in analysis of serum, urine and biopsy, particularly during and after the reserved in the solution and solution and solution and solution and solution and serum, urine and biopsy, particularly during and after the reserved in the solutions of the solution and solutions and astronced as a markers for analysis of serum, urine and biopsy, particularly during and after the reserved as the solutions and serum, urine and biopsy, and Abal2081 and A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent sequence used in the exemplification of the present invention.
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Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 other;

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The present invention describes an lipopolysaccharide (LPS) activated human monocyte expression gene group consisting of the higheranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LPS in which the CDNA of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3' nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various human diseases in which human monocyte plays an important role.

AAH33628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH32944
human monocyte expression gene group consisting of the high-ranking 50 genes of the highest expression among the genes expressed by human monocyte stimulated by LDS in which the CDNA of each gene has the base sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-CATG-3' nearest to the polyA region. The gene group is useful for the development of new means for the diagnosis and the treatment of various human diseases in which human monocyte plays an important role. AAH32628 to AAH32943 represent specifically claimed LPS activated human monocyte expression gene cDNA tags from the present invention. AAH33944 represents an LPS activated human monocyte expression gene cDNA sequence encoding AAB98009, which are given in the exemplification of the present
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No.3
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Matches
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences shaf63161-AAM64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                    ome; gene expression pattern; cancer; drug screening; cell specific gene expression; ss.
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                                                                                                                                                                                                                                                                         Human ubiquitously expressed transcriptome sequence SEQ ID NO: 435.
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                             Gaps
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Length 10;
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Pred. No. 3
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42.0%;
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                            9; Conservative
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particular cell types
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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aah63595
                             Matches
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Vogelstein B,
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90.0%;
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         transcriptome;
diagnosis; cel
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Matches 9; Conserv
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                                           Homo sapiens
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           Human;
                    cancer
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aai67389/c
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                                                                                                                                                   transcriptome; gene expression pattern; cancer; drug screening; diagnosis; cell specific gene expression; ss.
                                                                                                                               Human colon cancer associated transcriptome sequence SEQ ID NO: 1496
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                                                                                                                                                                                                                                                                                                                                                             polynucleotides, useful for identifying specific cancer cell, comprises transcriptomes expressed
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                                          from: 1
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                                                              AAH64656 standard; cDNA; 10 BP
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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particular cell types
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                     RESULT 36
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAM63161-AAM64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention.
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       cancer; drug screening;
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ome; gene expression pattern; cancicell specific gene expression; ss
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Pred. No. 30
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Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal; CHRNB2; memory disorder; Alzheimer's disease; epilepsy; learning; chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder; ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADNFLE; ss; allele specific oligonucleotide; ASO; PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an individual involves determining for two copies of the gene, the identity of nucleotide pair at polymorphic sites selected from PSI-24
                                                                                               (SNPS) in the human myeloproliferative leukaemia virus oncogene (MPL) gene located on chromosome 1p34, and methods for haplotyping and/or genetyping the MPL gene. The methods of the invention make use of allele-specific oligonucleotides (ASOS) as probes and primers and/or primer-extension oligonucleotides for detecting MPL gene polymorphisms. The polynucleotides and screened compounds are useful for the treatment of diseases associated with MPL activity, such as congenital amegakaryocytic thrombocytopaenia (CAMT).
AAS19570-AAS19607 represent primer-extension oligonucleotides for detecting human MPL gene polymorphisms.
                                                                             present invention relates to novel single nucleotide polymorphisms
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                                       Claim 17; Page 16; 85pp; English.
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2000US-217952P.
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90.0%;
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Matches 9; Conservative
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13-JUL-2000;
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MPL activity
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                                                                                                                                                                                                                                                                                            The invention relates to haplotyping the FK506-binding protein 8 (38KD) (FKBP8) gene in an individual. The method involves determining the identity of the nucleotide pair at one or more polymorphic sites selected from P1 to P26 (described in the specification). The invention is useful to improve the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with FKBP8 activity, for example immunosuppression and cancer. Sequences AAI67352-403 represent oligonoucleotide primers for detecting FKBP8 gene polymorphisms by primer extension techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer-extension oligonucleotide #7 to detect human MPL polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34; myeloproliferative leukaemia virus oncogene; haplotyping; genotyping; congenital amegakaryocytic thrombocytopaenia; CAMT; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA167389 Length: 10 October 2, 2003 14:57 Type: N Check: 3735
                                                                                                                                                                    New haplotypes of the FK506-binding protein 8 gene, useful for genotyping that gene in individual and to design new therapy associated disease such as immunosuppression and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                  Koshy B;
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                                                                  Kliem SE,
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                                                                  Choi JY,
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                                                                                                                                                                                                                                                             Claim 16; Page 15; 98pp; English.
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                                                                  Bentivegna SC,
                        (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001WO-US12301.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                    Anastasio AE,
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                                                                                        Stephens JC;
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polymorphic DNA (RAPD) reaction in the assay of the invention. This assay is used to determine if an animal has an allele for, or muscle fibre composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce meat of superior quality (particularly tenderness) but are normally less efficient feed converters and fatter than other types. The assay comprises analysing a tissue sample to determine if the genotype comprises the allele, and genetic features typical of animals with Duroc-type MFC are present. The method is used to select animals that have Duroc characteristics for use in breeding programmes (to develop the animals with Duroc pig characteristics), and to assess meat quality.
        Assay for alleles or muscle fibre composition characteristic of Duroc type pigs - comprises determination of genotype or muscle fibre properties, used to identify animals for breeding programs and to assess meat quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                    PCR primers AAV35877-996 were used in a rapid amplification of
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Pred. No. 30;
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                                                                                                            Example 3; Page 32; 56pp; English.
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Best Local Similarity 90.0
Matches 9; Conservative
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(SHAN/) SHANKARA S.
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19-JUN-1998;
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comprising determining for the two copies of the CHRNB2 gene present in the individual, the identity of the nucleotide pair at one or more to the individual, the identity of the nucleotide pair at one or more polymorphic sites selected from PS1-24. Also include are oligonucleotides for performing the method and the nucleotide sequence of the polymorphic variants of CHRNB2. The method is useful for detecting novel CHRNB2.

Co polymorphisms and for determining if an individual has a haplotype or palymorphisms and for determining if an individual has a haplotype or candidate agent for treating a specific condition or disease predicted to composite with CHRNB2 activity (e.g. a memory disorder, Alzheimer's disease, epilepsy, a learning disorder, schizophrenia, attention deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal frontal lobe epilepsy (ADMFLE)), and in the design of clinical trials of candidate drugs for treating a specific condition or disease from compounds targeting CHRNB2 activity. The method is useful to screen for compounds targeting CHRNB2 to treat a specific conditions or disease associated with CHRNB2 activity. The method is useful to expressing CHRNB2 protein for use in screening for candidate drugs to treat diseases related to CHRNB2 activity and are useful for therapeutic current diseases related to CHRNB2 activity and are useful for therapeutic sequence is an allele specific oligonucleotide (ASO) PCR primer (3' terminus) for performing the method of the invention.
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Pred. No. 30;
0; Mismatches 1; Indels
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96GB-0020904.
97GB-0003350.
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90.0%;
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Best Local Similarity 90.(
Matches 9; Conservative
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aaz84309
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                                              transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour rissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic genes. Therapeutic genes cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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; TOIG of: aaz83550 check: 3859 from: 1
   prevention and treatment of cancer
                            Claim 1; Page 129; 219pp; English.
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98US-0090039.
98US-0090040.
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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(ROBE/) I
(SHAN/) 3
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transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast transcripts. The transcripts that are upregulated in metastatic breast transcripts.

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour fissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive immunotherapy.
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Roberts BL, Shankara S;
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23-DEC-1999
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AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells).

AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense cell types, of e.g. therapeutic genes (also ribozymes or antisense cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic genes. Cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter.
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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98US-0090039,
98US-0090040,
98US-0090041.
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                              (SHAN/) SHANKARA S.
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19-JUN-1998;
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transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

AAZ83942 to AAZ8667 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells).

Dreast tumour tissue (i.e. are downregulated in metastatic breast tumour cells).

Mentast tumour tissue (i.e. are downregulated in metastatic breast tumour properties transcripts can be used for diagnosis, prognosis, monitoring and treatment of metastatic particularly where metastatic biagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense cell-based vaccines; for diagnosing breast cancer and for raising useful in vaccines; for diagnosing breast cancer and for raising
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be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention and treatment of cancer
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                                                                                                 98US-0089997.
98US-0090039.
98US-0090040.
98US-0090041.
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transcripts that are preferentially transcribed in the metastatic breast
tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
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breast tumour tissue (i.e. are downregulated in metastatic breast tumour
cells). These transcripts can be used for diagnosis, prognosis,
conjuding and treatment of breast cancer, particularly where metastatic.
Diagnosis is by standard immunoassays or hybridisation/amplification
reactions. Compounds that modulate expression of the transcripts are
potentially useful for treatment of (metastatic) breast cancer, while
coll types, of e.g. therapeutic genes (also ribozymes or antisense
sequences), particularly an antigen-encoding sequence for use in gene or
cell-based vaccines; for diagnosing breast cancer and for raising
specific antibodies (Ab). Ab are used to detect the polypeptides or as
therapeutic genes.
Co expand and isolate populations of educated, antigen-specific immune
confector cells, e.g. cytotoxic I lymphocytes, and these used for immune
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Human; metastatic breast tumour tissue; breast cancer; tag; p;
non-metastatic breast tumour tissue; gene therapy; anticancer,
antimetastatic; vaccine; diagnosis; ss.
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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transcripts that are preferentially transcribed in the metastatic breast tumour tissue (1.e. are upregulated in metastatic breast tumour tissue (1.e. are upregulated in metastatic breast tumour cells).

AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downrequiated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences); particularly an antigen-encoding sequence for use in gene or useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as the propagation of particularly an antigen-encoding sequence for use in gene or useful in vaccines; for diagnosing breast cancer and for raising the propagation of particularly and particularly and particularly and particularly and parti
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                                                                                       Metastatic breast tumour cell downregulated transcript tag #4825.
                                                                                                                                                                                                                   non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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98US-0090040.
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Matches 9; Conservative
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19-JUN-1998;
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The invention relates to a human normal hepatocyte expression gene group comprising 200 genes in the human normal hepatocyte. The CDNA of each gene comprises one of 200 fully defined nucleotide sequences as given in the specification. The gene group and the cDN corresponding to each of the genes in the group are useful in the diagnosis and treatment of human hepatopathy. The present sequence is a CDNA corresponding to a gene expressed by normal human
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                         Score 8.4; DB Pred. No. 30; 0; Mismatches
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AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected promoters from the transcripts are used to direct expression, in selected call types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising consisting and present and for raising consisting and antigen are and consisting and consisting are also consisting and consisting consisting and consisting consisting and consisting consist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis,
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                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a nucleic acid library comprising myc-dependent downstream genes or their functional fragments essentially capable of supporting a neoplastic character of cancer such as growth, invasion or spread. These myc target or tag sequences are identified by SAGE (serial analysis of gene expression). The library is useful to find new diagnoses and treatments for cancer. The invention is also useful to enhance production of recombinant proteins in a production system with high expression of endogenous or transfected myc oncogenes. ABX23412-ABX23828 represent transcript tag DNA sequences that are activated or repressed by N-myc in human neuroblastoma.
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                                                                                                                                                                                                                                                                                  ary of myc-dependent downstream genes capable of characteristic of cancer is useful to find new
                               Myc-dependent downstream gene; neoplastic; cancer; growth; invasion; spread; myc target; myc tag; SAGE; serial analysis of gene expression; myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
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            Transcript tag DNA sequence #2 induced or suppressed by N-myc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; small inducible cytokine subfamily B (Cys-X-Cys); Member 6 (granulocyte chemotactic protein 2); SCYB6; primer; infilammatory disorder; cancer; antiinfilammatory; cytostatic; gene therapy; SCYB6 isogene expression modulator; SNP; single nucleotide polymorphism.
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                                                                                                                                                                                                              (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                             supporting a neoplastic characteris
therapies and diagnoses for cancer
                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 49; 69pp; English.
                                                                                                                                                      11-MAY-2001; 2001WO-NL00361.
                                                                                                                                                                            2000EP-0201698
2000EP-0202284
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                                                                                                                                                                                                                                                                                    nucleic acid library
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                                                                                                                                                                                                                                      Caron HN;
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                                                                                                       WO200185941-A2.
                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                      Versteeg R,
                                                                                                                              15-NOV-2001
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Matches
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The present invention relates to a new polynucleotide having small inducible cytokine subfamily B (Cys-X-Cys), Member 6 (granulocyte chemicatic protein 2) (SCYB6) isogene. The invention is useful for studying expression and function of SCYB6 and expressing SCYB6 protein for use in screening for candidate drugs to treat diseases related to SCYBG activity. The polymorphism and haplotype data is useful for validating whether SCYB6 is a suitable target for drugs to inflammatory disorders and cancer, screening for such drugs and reducing bias in clinical trials of such drugs. The invention is also useful for the appendic purposes. The method of the invention is useful for identifying an association between susceptibility to a disease, staging of a disease, or response to a drug. The present nucleic acid sequence represents one of a collection of oligonucleotide primers (ABK85680-The human SCYB6 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polymorphic variant of small inducible cytokine subfamily B (Cys-X-Cys), Member 6 (granulocyte chemotactic protein 2) gene, useful for expressing protein isoform used in drug screening techniques
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                     Monroe G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                     Bentivegna SC,
                                                                                                                                                                                                                                                      (GENA-) GENAISSANCE PHARM INC
                                                                                                                           27-SEP-2001; 2001WO-US30413.
                                                                                                                                                                                          27-SEP-2000; 2000US-235809P.
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Best Local Similarity 90.0
Matches 9; Conservative
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WO200227030-A1.
                                                                                                                                                                                                                                                                                                                     Anastasio AE,
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JP2001327293-A.
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                                                                                                                                           The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/activation DC. Also described are: (1) a protein expressed by the above human maturation/activation C expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human DC. ABL42247 represent specifically claimed human maturation/activation DC expression gene tags from the present invention.
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                  Human maturation/activation dendritic cell expression gene group
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                                                      (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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          22-MAY-2000; 2000JP-0150562
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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ab142689
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The present invention describes a human maturation/activation dendritic cell (DC) expression gene group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human DC. ABL42627 to ABL4296 represent specifically claimed human maturation/activation DC expression gene tags from the present invention.
highest expression among the genes expressed in human maturation/ activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the DC. ABL42627 to ABL42262 represent specifically claimed human maturation/activation DC expression gene tags from the present invention.
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Pred. No. 30;
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90.0%;
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Best Local Similarity
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Length 10;

DB 1;

Score 8.4;

42.08;

Gaps

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Length 10; Indels

DB 1;

Score 8.4; DB Pred. No. 30; 0; Mismatches

42.0%;

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Query Match 42.0
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                Gaps
                                                                                                                                                                                                                                        Zinc finger protein related oligonucleotide target SEQ ID NO:1270.
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                Indels
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 Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                            BP.
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90.08;
               Conservative
                                        3316 GGATTCAGGG 3325
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                                                               10 GGATCCAGGG 1
 Best Local Similarity
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                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                              8-AUG-2002
                                                                                                                                                                                                                                                                                                                                                           30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-terminus
                                                                                                                                                                                     ABQ71536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu O;
                                                                                                    RESULT 55
abq71536
               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abq71536
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The present invention describes a zinc finger protein (1) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from W-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynuclectide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that binds to the S2 target subsite, thus designing (I) that binds to the S2 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human the subject, in diagnostic methods for sequence specific detection of a subject, in diagnostic methods for sequence specific detection of the subject, in diagnostic methods for sequence specific detection of subject, in diagnostic methods for sequence specific detection of the subject, in diagnostic methods for sequence specific detection of subject, in diagnostic methods for sequence specific detection of sequences, as well as enhanced the biological activity. ABQ71213 to ABB71214 and ABB48191 to ABB51230 the second in the process and zinc finger peptides which are given in the avamant fination of the process and zinc finger peptides which are given in the second second for sequence and zinc finger and specific detection of grant function of the process and zinc finger peptides which are given and the process and zinc finger peptides which are given and specific detection of the process and zinc finger peptides which are given and specific detection of the process and zinc finger and specific detection of the process and zinc finger and specific detection d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein related oligonucleotide target SEQ ID NO:1275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                          to: 10
                                                                                                                                                                                                                                                                                                                                                                          check: 3978 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2001; 2001WO-US43438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-2000; 2000US-0716637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ71541 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
3314 AGGGATTCAG 3323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-500284/53.
                                                                                                    ATGGATTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200242459-A2.
                                                                                                                                                                                                                                                                                                                                                                     TOIG of: abq71541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ71541;
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Gaps

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Indels

Mismatches

Score 8.4; DB 1; Length 10; Pred. No. 30;

42.0%; 90.0%;

N Check: 3978

October 2, 2003 14:57 Type:

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Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 other;
                                                                                                                   Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                               3314 AGGGATTCAG 3323
                                                                                                                                                                                                     1 ATGGATTCAG
                                     ABQ71603 Length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6083695-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hardin PE,
                                                                                                                                                                                                                                                                                                                                                                                                 AAA80926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                  Query Match
                                                           abq71603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered FI). F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polymucleotide (III) encoding (I) or (II); and (S) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsider and when the province of the continual of the starget subsite and when the province of the continual of the starget subsite and when the province of the continual of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subsite. (1) is useful in studying gene function, and for human therapeutics and plant engineering. (1), (11) or (111) is useful in therapeutic methods to medulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (1) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ71214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          related oligonucleotide target SEQ ID NO:1337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
    October 2, 2003 14:57 Type: N Check: 3978
                                                                                                  6
                                                           Length 10;
                                                                                                  Indels
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                                                                                                                                                                                                                                                                                    to: 10
                                                             DB
                                                           Score 8.4; DB
Pred. No. 30;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                         ABQ71603 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2000; 2000US-0716637
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                             42.0%;
90.0%;
                                                                                  Best_Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                          3314 AGGGATTCAG 3323
                                                                                                                                                                  Zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-500284/53
  ; ABQ71541 Length: 10
abq71541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                ABQ71603;
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu Q;
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                                                                                                                                                                                                                                                               abq71603
                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing an unknown DNA molecule for the polymerase chain reaction and other primer processes comprises primer walking of octamer oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA80926 Length: 8 October 2, 2003 14:57 Type: N Check: 2610
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                                                                                                                                                                                                                                                                                                                                                                                                      Primer walking; octamer; primer; DNA sequencing; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 8; DB 1; Length 8;
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels

    A. thaliana primer walking octamer SEQ ID NO: 239.

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RESULT 58
aaa80926/c
; TOIG of: aaa80926 check: 2610 from: 1
                                                                                                                                 AAA80926 standard; DNA; 8 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0632782.
                                                                                                                                                                                                                                                                  24-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hardin SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-474852/41.
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nes 8; Conserv
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Matches
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to: 10

check: 3887 from: 1

(first entry)

δ g

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
                                                                                                                                Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                                                         Feast NORF gene SAGE tag oligonucleotide SEQ ID NO:2430.
                           AAF35691 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                       14-JUN-2000; 2000WO-US16223.
                                                                                                                                                                                                                                                                                                                                             SNINGO NING CORNS
                                                                                                                                                                                                       Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-061874/07.
                                                                                                                                                                                                                                    WO200077214-A2.
TOIG of: aaf35691
                                                                                                                                                                                                                                                                                                                                                                        Velculescu V,
                                                                                                                                                                                                                                                                                                                  16-JUN-1999;
                                                                               23-MAR-2001
                                                      AAF35691;
                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel genetic variants of human tumour necrosis factor (INF) alpha genes. The polymorphic variants are useful in studying the expression and function of TNF, in expressing TNF proteil for use in screening for candidate drugs to treat diseases related to TNP activity. The pharmaceutical compositions comprising TNF polymucleotide, an antisease oligonucleotide directed against one of the novel TNF isogenes, a polymucleotide directed against one of the novel TNF another compound that inhibits expression of the TNF isogene are useful for treating disorders affected by expression of the TNF isogene e.g. cancer, diabetes or inflammatory disorders. Sequences of the invention are also used in gene therapy. The present DNA sequence is a primer used to detect human TNF alpha gene polymorphisms.
                                                                                                                                                                                                                                                  Human; tumour necrosis factor; TNF alpha; cancer; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genetic variants comprising human Tumor Necrosis Factor alpha (TNF) isogene, useful for studying the expression and function of TNF and in screening for drugs to treat cancer, diabetes or inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD45882 Length: 10 October 2, 2003 14:58 Type: N Check: 3937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sausker EA;
                                                                                                                                                                                                                        Human TNF alpha gene polymorphism detecting primer #2.
                                                                                                                                                                                                                                                                  diabetes; gene therapy; cytostatic; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
o. 35;
                                                                                                               to: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denton RR, Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 40.0%; Score 8; DB 1 Local Similarity 100.0%; Pred. No. 35; es 8; Conservative 0; Mismatches
                                                                                                            TOIG of: aad45882 check: 3937 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 13; 66pp; English.
                                                                                                                                        AAD45882 standard; DNA; 10 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                           03-DEC-2001; 2001WO-US46947.
                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2000; 2000US-250918P.
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-698545/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3319 TTCAGGGG 3326
                 3314 AGGGATTC 3321
                                          AGGGATIC 1
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                                                                                                                                                                                                                                                                                                                     WO200260918-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentivegna SC,
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                             27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                08-AUG-2002.
                                                                                                                                                                    AAD45882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                  aad45882
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Kinzler K;

Vogelstein B,

99US-0335032

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (3) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a cycle captession varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate which modifies the captession comprising contacting human DNA with a probe which comprises contiguous nucleotides of a NORF gene whose expression varies at lace of the yeast gene is a candidate drug as a captession of a noting nucleotides of a NORF gene whose expression varies contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a candidate drug and monitoring expression in the yeast cell of at least candidate drug and monitoring expression in the yeast cell of at least candidate drug and monitoring expression in the yeast cell of at least condidate drug and monitoring expression in the yeast cell of the cell cycle, the cilcycle and for identification of antifungal drugs.

Che differentially expressed genes may be used as markers of phases of the cell cycle and for identification of antifungal drugs.

AMF33268 to AAF44064 represent sAGE tags used in the exemplification of the present invention. AAF33267 represent linkeds and PCR considered in the SAGE method, in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 2, 2003 14:58 Type:
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Example; Page 86; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF35691 Length: 10
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DB 1; Length 10;

Score 8; DB 1 Pred. No. 35;

40.0%; 8

Query Match Best Local Similarity

RESULT 60 aaf35691

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invention.
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          Gaps
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       Indels
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   Mismatches
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   Conservative
                                                                 3324 GGGTTCCA 3331
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   Matches
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonannotated ORF) genes coding sequence of a yeast gene selected from the control of the comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contracting a test substance with a cypression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies at least 10 contiguous nucleotides of a NORF gene whose expression varies at least 10 contiguous nucleotides of a north of a class of drugs having a characteristic effect on gene comprised to a class of drugs having a characteristic effect on gene expression in a yeast cell with a
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                                                                                                                                            Gaps
                                   AAF36466 Length: 10 October 2, 2003 14:58 Type: N Check: 3858
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Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 other;
                                                                                                Score 8; DB 1;
Pred. No. 35;
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                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                           RESULT 62
aaf40055/c
; TOIG of: aaf40055 check: 3949 from: 1
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                                                                                40.0%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae.
                                                                          Query Match
Best Local Similarity 100.0
                                                                                                                                                                            3325 GGTTCCAG 3332
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                                                                                                                                                                                                                    8 GGTTCCAG 1
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candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAR33268 to AAR44064 represent SAGE tags used in the exemplification of the present invention. AAR33262 to AAR33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present
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                                                                                                                                                                                                                                                                                                          Length 10;
                                                                                                                                                                                                               Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                                          DB 1;
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100.0%;
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Best Local Similarity 100...
8; Conservative
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                                                                                                                                                                               invention.
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expression varies as in MJ, where a test substance which modifies the expression varies as in MJ, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in MJ; and (4) a method (M4) for identifying a candidate drug as a capression in a yeast cell comprising contacting a yeast cell with a captression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell of at least NORF gene whose expression is affected by the class of drugs. The NORF condidate drug and monitoring expression in the yeast cell of at least confidence in such contact and affect phases of the cell cycle, confidentification of antifungal drugs.

Condidate cell cycle and for identification of antifungal drugs.

AAF33268 to AAF43061 captessed in the exemplification of the present
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100.0%; Pred. No. 35;
tive 0; Mismatches
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Matches 8; Conservative
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Control sequence or a yeast gene selected from a group or 43 work (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose cypression varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle cycle contiguous nucleotides of a NORF gene whose expression varies at least 10 contiguous nucleotides of a NORF gene whose expression in a yeast cell of at least 10 condidate drugs having a characteristic effect on gene expression in a yeast cell omprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 10 NORF gene whose expression is affected by the class of drugs which candidate drug and monitoring expression in the yeast cell of at least 10 Contiguous and provided the cell cycle. The methods may be used to identify candidate drugs which the cell cycle. The methods may be used to identify candidate drugs which the present invention. AAP33262 to AAP33264 frepressent linkers and PCR the primers used in the SAGE method, in the exemplification of the present
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present invention describes an isolated DNA molecule comprising a ng sequence of a yeast gene selected from a group of 745 NORF (not
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a cyeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate which modifies the expression varies as in M1, where a test substance which modifies the cypression comprising contacting human DNA with a probe which comprises to progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 10 NORF gene whose expression is affected by the class of drugs. The NORF contacting a markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. C the differentially expressed genes may be used as markers of phases of the cell cycle and for identification of antifungal drugs. C the primers used in the SAGE method, in the exemplification of the present invention. AAPF33262 to AAF$3267 represent linkers and principle or the resent linkers and principle or the resent linkers or the drugs which invention.
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                                                                  Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
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35;
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                               Example; Page 334; 419pp; English.
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention.
Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                        cell
in
                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotides, useful for identifying specific type, such as cancer cell, comprises transcriptomes expressed particular cell types -
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ilarity 100.0%; Pred. No. 35;
Conservative 0; Mismatches
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Best Local Similarity
Local 8; Conserve
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                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, 5 phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a cycast cell; and (b) monitoring expression of a NORF gene whose expression varies as in M1, where a test substance which modifies the expression varies as in M1, where a test substance which modifies the cypression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene member of a class of drugs having a characteristic effect on gene candidate drug and monitoring expression in the yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 10 NORF gene whose expression is affected by the class of drugs. The NORF comparison is affected by the class of drugs which candidate drug and monitoring expression in the yeast cell of at least 10 candidate and for identifying a candidate drugs which cafferentially expressed genes may be used to identify candidate drugs which the cell cycle. The methods may be used to identify and drugs. CAAF33268 to AAF43268 to identification of antifungal drugs.

CHAF33268 to AAF43664 represent SAGE method, in the exemplification of the present invention. AAF33267 to present linkers and PCR invention.
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                                                                                                                                                                                                                   Yeast gene coding sequences comprising NORF genes with serial analys of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle -
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                                                                                                                                          Velculescu V, Vogelstein B,
                                14-JUN-2000; 2000WO-US16223.
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nes 8; Conserv
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                                                                     16-JUN-1999;
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21-DEC-2000
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Matches
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The sequences given in AAQ65549-60 are spacer elements used within the insertion elements of the invention. These insertion elements contain junk DNA, two spacer elements, a functional DNA sequence and a primer binding site. They also contain an MluI site, an MluI site, an MluI site ire and a NheI site. The junk DNA serves to keep the MluI site from being at the extreme end of the molecule and also allows determination that the MluI cleavage has occured because the extended DNA will be reduced in size by the length of the junk sequence and the junk sequence will appear as a reaction product. The junk sequence will appear as a reaction product. The junk sequence will appear as a reaction product. The junk sequence will appear use thosen randomly and the functional nucleotides sequence is chosen to achieve the binding site can be synthesised. However, the primer binding site can be synthesised. However, the primer and primer binding site are chosen such that the primer itself does not brind to any other portion of the insertion element under construction. Consertion sequences such as these can be used to insert a functional molecule into a host molecule to form a recombinant molecule. The spacer elements are thought to relieve structural stresses imposed on the host by addition of the functional nucleotide sequence. The host by addition of the functional nucleotide sequence. The host by addition of the functional nucleotide sequence. The host be used with nucleic acid hybridisation assays. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                           Insertion elements and amplifiable nucleic acids - for use as probes in hybridisation assays and for the prepn. of libraries used to identify preferred insertion elements.
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0; Mismatches
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92US-0959939.
93US-0045587.
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                                                                (STAD ) AMOCO CORP.
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09-OCT-1992;
09-APR-1993;
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Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cells other transcripts correspond to novel genes. Antigen-presenting cells. (APC) associated costimulatory factors play an important role in the activation of the cytocoxic immune response that can cells. Tumour antigen presentation via the MMC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytocoxic T-lymphocytes (CTLS). Nucleic activation of cytotoxic T-lymphocytes (CTLS). Nucleic active may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hyporidisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and
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98US - 0089853
98US - 0089991
98US - 0089991
98US - 0089999
98US - 0089999
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98US - 0090000
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98US - 009007
                                  99WO-US13800
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RESULT 71
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vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells.
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immunostimulatory cofactor; costimulatory factor; CTL;
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o. 35;
                                                                Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 other;
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                                                                                                          40.0%; Score 8; DB 1
100.0%; Pred. No. 35;
Live 0; Mismatches
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nes 8; Conservative
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Matches
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Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell (APC) assocified costimulatory factors play an important role in the cativation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MMC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can complex) and subsequent recognition by T-cell receptors is alone insufficient activation of cytotoxic r-lymphocytes (CTLs). Nucleic acid for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid gainst a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes. Or of their encoded proteins, can be used in vaccines to induce an immune response, particularly expressed genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate the dendritic cell differentially expressed genes, or of their encoded proteins, cells containing them are used in gene therapy. Co-administration of vectors containing them are used in gene therapy. Co-administration of vectors containing them are used in gene therapy. Co-administration of vectors containing them are used in gene therapy. Co-administration of co-stimulatory signals, migration of chemokines for the presentation of co-stimulators and secretion of co-stimulators and secretion of co-stimulators and secretion of cells containing them are us
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tive 0; Mismatches
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98US-0090080.
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19-JUN-1998;
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Sequences AAZ77573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell cher transcripts correspond to novel genes. Antigen-presenting cell cher transcripts correspond to novel genes. Antigen-presenting cell chery factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid
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                            SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL;
                                                                          cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
dendritic cell SAGE tag, SEQ ID NO:1337.
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98US-0090041.
98US-0090042.
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                                                                                                        Homo sapiens.
                                                                                                                                  WO9965924-A2.
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19-JUN-1998;
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sequences identified using the SAGE tags have several potential uses.
They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and the production of a population of antigen-specific effector cells) and cumour antigens and APC associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of or estimulatory signals, migration to T cell-rich sites, secretion of I cell growth factors and secretion of chemokines for recruitment of immune effector cells.
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches
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98US-0089997.
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                                                                                                                                                 reactions. Compounds that mindlate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for
                                   AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoasays or hybridisation/amplification
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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               Claim 1; Page 83; 219pp; English.
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100.0%; Pre
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98US-0090039.
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Best Local Similarity 100.
Matches 8; Conservative
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast transcripts. The transcripts that are upregulated in metastatic breast transcripts.

AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour fissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoasays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or eacli in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expend and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive immunotherapy.
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                  Isolated polynucleotides differentially expressed between met and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
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40.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches
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aaz83968/c
; TOIG Of: aaz83968 check: 3832 from: 1 'to: 10
                                                                                                                                                                                                                                                                                       Claim 1; Page 101; 219pp; English.
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Roberts BL, Shankara S;
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SAN TANKARAN TANKARAN
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AAX83942 to AAX86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells).

Decast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridiation/amplification reactions. Compounds that modulate expression of the transcripts are promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense cell types, of e.g. therapeutic genes (also ribozymes or antisense cell types, of e.g. therapeutic genes (also ribozymes or antisense cell) particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising therapeutic agents. Host cells that produce the polypeptides on as therapeutic agents. Host cells that produce the polypeptides on as therapeutic agents. Host cells that produce the polypeptides can be used to effecte cells, e.g. cytotoxic I lymphocytes, and these used for
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                             prevention and treatment of cancer
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  98US-0090040
98US-0090041
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                                                                                                                                                                                              Shankara
                                                                             (GENZ ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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aaz84127
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transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast transcripts.

AA283942 to AA286677 represent tags corresponding to distinct transcripts.

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour calls).

Collish. These transcripts can be used for diagnosis, prognosis, and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell. types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell.based vaccines, for diagnosing breast cancer and for raising useful in vaccines; for diagnosing breast cancer and for raising therapeutic agents. Host cells that produce the polypeptides on as therapeutic capents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer -
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98US-0090041.
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Matches 8; Conservative
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19-JUN-1998;
19-JUN-1998;
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AAZ84158;
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transcripts that are preferentially transcribed in the metastatic breast
tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

AA283942 to AA286677 represent tags corresponding to distinct transcripts
that are preferentially transcribed in the primary or non-metastatic
transcripts can be used for diagnosis, prognosis,
monitoring and treatment of breast cancer, particularly where metastatic.
Diagnosis is by standard immunoassays or hybridiation/amplification
reactions. Compounds that modulate expression of the transcripts are
promoters from the transcripts are used to direct expression, in selected
cell types, of e.g. therapeutic genes (also ribozymes or antisense
cell types, of e.g. therapeutic genes (also ribozymes or antisense
cell-based vaccines; for diagnosing breast cancer and for raising
specific antibodies (Ab). Ab are used to detect the polypeptides or as
therapeutic agents. Host cells that produce the polypeptides can be used
to expand and isolate populations of educated, antigen-specific immune
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 non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
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                                                                                                                                                                                                             SHANKARA S.
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                                  Homo sapiens
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AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation, and principle and present the contraction of the contraction 
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useful for diagnosis,
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                                                                                                               Metastatic breast tumour cell downregulated transcript tag #3392
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                                                                                                                                                                                                                                                  Human; metastatic breast tumour tissue;
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Pred. No. 35; Mismatches

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Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
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                                                                                                                                                                                                                                    Human; metastatic breast tumour tissue; breast cancer; tag; primer;
                                                                                                                                                                                               Metastatic breast tumour cell downregulated transcript tag #3491.
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                                aaz84257/c
; TOIG of: aaz84257 check: 4042 from: 1
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                                                                                       AA284257 standard; DNA; 10 BP.
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DB 1; Length 10;

40.0%; Score 8;

Query Match

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transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells).

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells).

AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to discret expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.
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                                                                                                                                                                                      Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer;
                                                                                                                                                      Metastatic breast tumour cell downregulated transcript tag #3635.
                                                                                                                                                                                                                 non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
to: 10
TOIG of: aaz84401 check: 3887 from: 1
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                                     AAZ84401 standard; DNA; 10 BP.
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AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis,
cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be use to expand and isolate populations of educated, antiger specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.
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                                                                                                                                                            ; AAZ846B5 Length: 10 October 2, 2003 14:58 Type: N Check: 4063 aaz84685
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Pred. No.
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; TOIG of: aaz85131 check: 3877 from: 1
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Matches 8; Conservative 0;
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transcripts that are preferentially transcribed in the metastatic breast
twoour tissue (i.e. are upregulated in metastatic breast transcripts
that are preferentially transcribed in the primary or non-metastatic
breast tumour tissue (i.e. are downregulated in metastatic breast tumour
cells). These transcribts can be used for diagnosis, prognosis,
monitoring and treatment of breast cancer, particularly where metastatic.
Diagnosis is by standard immunoassays or hybridisation/amplification
reactions. Compounds that modulate expression of the transcripts are
potentially useful for treatment of (metastatic) breast cancer, while
promoters from the transcripts are used to direct expression, in selected
cell types, of e.g. therapeutic genes (also ribozymes or antisense
sequences), particularly an antigen-encoding sequence for use in gene or
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non-metastatic breast tumour tissue; gene therapy; anticancer;
antimetastatic; vaccine; diagnosis; ss.
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monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in the metastatic breast transcripts that are preferentially transcribed in metastatic breast tumour calls).

AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cast tumour tissue (i.e. are downregulated in metastatic breast tumour cast tumour tissue of breast cancer, particularly where metastatic biagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected call types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising encodines, the publication is need to direct expression, in selected call-based vaccines, for diagnosing breast cancer and for raising encodines, and the pression of the transcripts are also ensed to antition of pressing encodines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific antibodies (Ab). As are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be use to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive immunotherapy.
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100.0%; Pred. No. 35;
tive 0; Mismatches
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Matches 8; Conservative
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Homo sapiens.
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                        This invention relates to genetic variants of the human related RAS
viral oncogene RRAS. Ras proteins are a member of a superfamily of small
GTPasses that are involved in the regulation of cell growth. The
invention also comprises a related RAS viral (r-ras) oncogene homologue
invention also comprising one or more of the polymorphisms shown.

(RRAS) isogene comprising one or more of the polymorphisms shown.

RRAS or to treat disorders such as cancer using antisense therapy.

The sequences of the invention is useful for providing
haplotype information of an individual. Furthermore, the polymorphic
sequence is useful for studying the biological function of RRAS as well
as identifying drugs targeting the protein for the treatment of
disorders related to its abnormal expression or function. In particular
for validating whether RRAS is a suitable target for drugs to treat
cancer, screening for such drugs and reducing bias in clinical trials.

The present sequence represents an allele specific oligonucleotide
primer #15 used to detect the human related RAS viral oncogene (RRAS)

Primer #15 used to detect the human related RAS viral oncogene (RRAS)
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Pred. No. 35;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                      Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 other;
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Claim 18; Page 12; 60pp; English.
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Best Local Similarity 100.0%;
Matches 8; Conservative 0
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The present invention relates to a nucleic acid library comprising myc-dependent downstream genes or their functional fragments essentially capable of supporting a neoplastic character of cancer such as growth, invasion or spread. These myc target or tag sequences are identified by SAGE (serial analysis of gene expression). The library is useful to find new diagnoses and treatments for cancer. The invention is also useful to enhance production of recombinant proteins in a production system with high expression of endogenous or transfected myc oncogenes. ABK23412-ABK23828 represent transcript tag DNA sequences that are activated or repressed by N-myc in human neuroblastoma.
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                                                                                                                                                                                                                                                                                                                                                 Score 8;
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29-JUN-2000; 2000EP-0202284.
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Best Local Similarity 100.00
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Primer-extension oligonucleotide #9 to detect human ADORA3 polymorphisms.
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                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;
chromosome 1p21-p13; adenosine A3 receptor; genotyping;
pathophysiological heart condition; myocardial ischaemia;
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                                                                   N Check: 3877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel genetic variants of the adenosine A3 receptor, useful therapeutically and in screening for drugs to treat diseases ADORA3 activity e.g., myocardial ischaemia and chronic heart
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 or repressed by N-myc in human neuroblastoma
                                                                                                                    Length 10;
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Pred. No. 35;
0; Mismatches
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Best Local Similarity 100.0%;
Matches 8; Conservative 0
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Query Match

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The invention federes to a polynuciectude compitising a filts, nucleotide sequence (NSI) comprising a PLAU (plasminogen activator, urokinase, a serine protease) isogene selected from isogene activator, urokinase, a serine protease) isogene selected from isogenes 1-9 and 11-20 given to the protease isogene comprises the regions of the PLAU gene or converse the regions of the PLAU gene polymorphisms, SNR). Also included are methods of haplotyping/genotyping (and predicting the haplotype/genotype of the PLAU gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the PLAU gene, a recombinant non-human organism configuration between a trait and at least one haplotype or haplotype pair of the PLAU gene, a recombinant non-human organism cransformed or transfected with the gene or CDNA, fragments of the polynucleotides of at least 10 base pairs encompassing a polymorphic colynaciblic variant PLAU gene or CDNA, a computer system for isolated monoclonal antibody specific for PLAU, a computer system for storing and analysing polymorphic variant PLAU gene and a genome contained plan that the PLAU gene. PLAU is useful in screening for drugs attached monoclonal antibody specific for PLAU, a computer system for cargeting PLAU that are useful for improving the efficiency and cancers. The methods are useful for improving the efficiency and disease associated with PLAU activity, in validating PLAU as a drug cancers. The methods are useful for improving the activity, the antibody is condition of disease associated with PLAU activity, the antibody is useful in diagnostic, prognostic and therapeutic methods. PLAU entition of polynucleotides are useful in studying the expression and function of
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; primer; Plasminogen activator; urokinase; PLAU; cancer; cytostatic; serine protease; thrombolytic disorder; isogene; PCR; pulmonary embolism; chromosome 10q24-qter; haplotype; genotype; SNP; single nucleotide polymorphism; thrombolytic; gene therapy;
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                  Pred. No. 35;
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100.08; Pr
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                                    8; Conservative
                                                                               3318 ATTCAGGG 3325
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               Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens,
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3320 TCAGGGGT 3327
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a method for the PCR amplification of nucleic acids. The method involves a set of primers, where two of the primers are in solution and at least two other primers are attached to a solid support. The method of the invention can be used for the analysis of a nucleic acid or a mixture of nucleic acids, including: single-stranded DNA molecules, double-stranded DNA molecules and mRNA molecules. The present DNA sequence represents a random amplified polymorphic DNA (RAPD)
                                                                                                                                                                                                                                                                                                                                                ö
         PLAU, and in expressing PLAU protein for use in screening for candidate drugs to treat diseases related to PLAU activity. The gene for PLAU is located on chromosome 10924-qter. The present sequence is the 3' terminus of an allele specific primer used to amplify PLAU polymucleotides with a specific polymorphism using the technique of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amplification of nucleotide sequences from polynucleotides by chain extension of oligonucleotide primers, comprises 2 oligonucleotides in solution, 2 attached to supports and both share complementary sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA analysis; ss;
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid amplification; nucleic acid analysis; BNA analysis; sRNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid PCR amplification method-related RAPD PCR primer #82.
                                                                                                                                                                                                                         October 2, 2003 14:58 Type: N Check: 3838
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                                                                                                                                                                           Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                         40.0%; Score B; Diarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                                                                                                   primer extension.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAGGGG
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This sequence represents the recognition site contained within the delta-globin promoter for the delta-EKLF (erythroid Krueppel-like factor) polypeptide (II) of the invention. DNA encoding (II) is used in gene therapy to induce delta-globin gene expression, particularly in haematopoietic cells, specifically for treating sickle cell anaemia and haematopoietic cells, specifically for treating sickle cell anaemia and beta-thabassemia. Increased expression of delta-globin increases production of the HbA2 form of haemoglobin which has anti-sickling activity. The DNA encoding (II) is introduced into cells in vivo or in measuring levels of (II) expression in treated patients. Since (II) is a transcription factor, lower quantities of it are required compared with other sorts of therapeutic gene products.
                                                                                                                                                                                                                                                                                            Delta-globin promoter; delta-EKLF; erythroid Krueppel-like factor;
gene therapy; haematopoietic cell; sickle cell anaemia; beta-thalassemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding an erythroid Krueppel-like factor that binds the delta-globin promoter - used in gene therapy to increase delta-globin expression for treatment of sickle cell anaemia and beta-thalassemia
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Pred. No. 2e+02;
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                                                                                                                                                                                                                                     Delta-EKLF polypeptide recognition site.
TOIG of: aav04711 check: 3169 from: 1
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                                                          AAV04711 standard; cDNA; 9
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88.9%;
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                                                                                                                    AAV04711;
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Search completed: October 2, 2003, 15:35:58 Job time : 1 secs